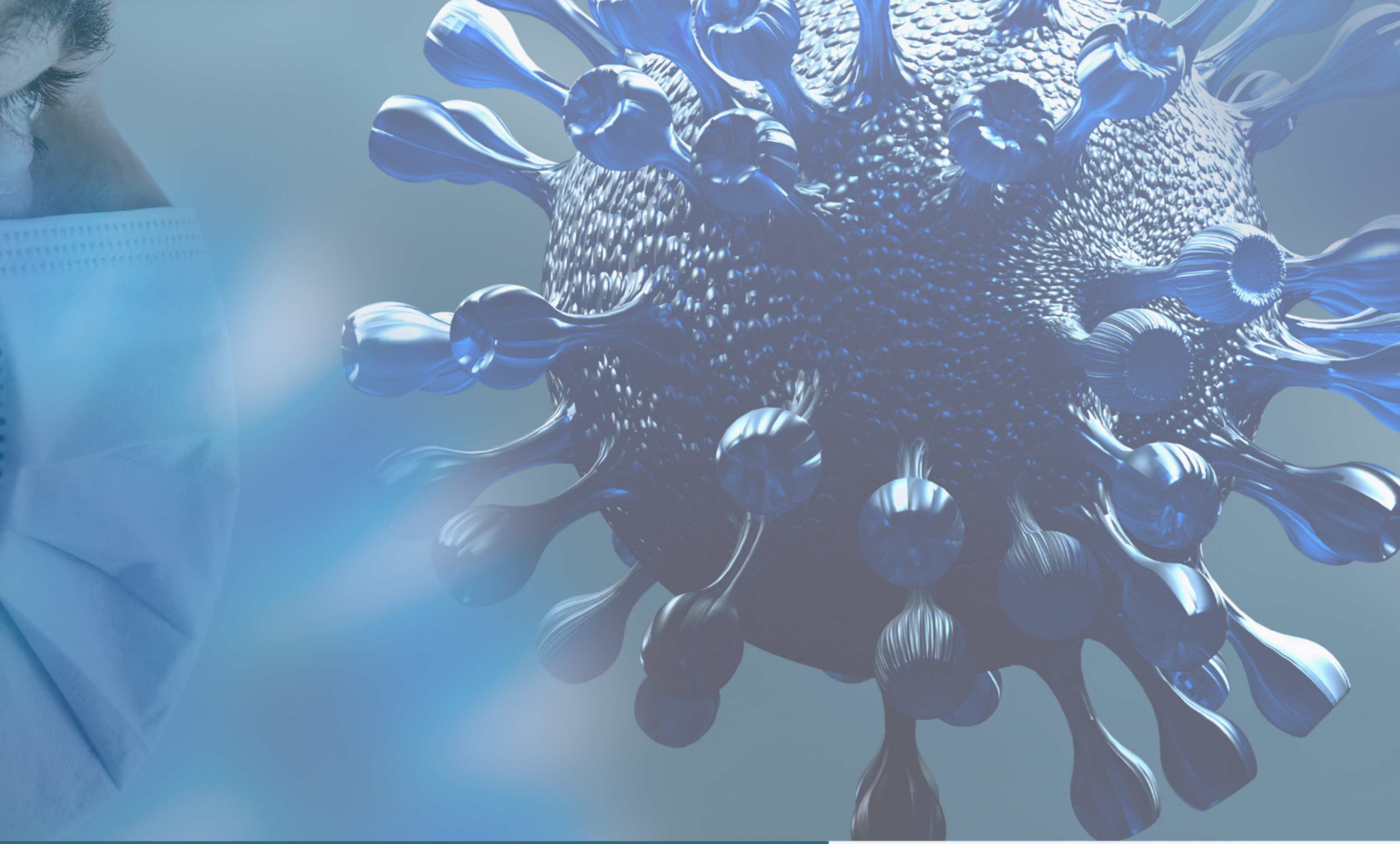


AUGUST 2021

THE ORIGINS OF COVID-19:

AN INVESTIGATION OF THE WUHAN INSTITUTE OF VIROLOGY

HOUSE FOREIGN AFFAIRS COMMITTEE
REPORT MINORITY STAFF

LEAD REPUBLICAN MICHAEL T. MCCAUL

ONE HUNDRED SEVENTEENTH CONGRESS

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INTRODUCTION

Five hundred and four days ago, on March 16, 2020, Committee Minority Staff began its investigation into the origins of SARS-CoV-2 and the COVID-19 global pandemic at the direction of Ranking Member Michael T. McCaul. The House Foreign Affairs Committee Minority Staff Final Report on The Origins of the COVID-19 Global Pandemic, Including the Roles of the Chinese Communist Party and the World Health Organization was published in late September 2020. At the time of its release, there were an estimated 30.8 million cases of COVID-19 around the world, and a death toll of approximately 958,000. Today, the cumulative count stands at more than 196.4 million cases and 4,194,061 dead.

The House Foreign Affairs Committee Minority Staff has continued to investigate the origins of COVID-19, examining new information as it became available, including through expert testimony. We have done so because approximately 48 million of our population are under the age of 12 and without access to a vaccination, while others remain unvaccinated due to underlying medical conditions, leaving a large portion of American citizens at risk of infection. We prepared this addendum as reports increase regarding various strains around the globe, and as PRC authorities continue to withhold critical information about the early months of the pandemic. We have strongly urged our Majority colleagues to take this investigation seriously and conduct a full bipartisan investigation into the origins of COVID-19, and will continue to do so. President Biden has said he wants to discover how the pandemic began, and it is our duty to the American people to use all the tools in our arsenal in pursuit of that goal. As always, we stand ready to address this and other foreign policy challenges together and in a bipartisan manner. We must not let up on pressing General Secretary Xi and CCP authorities for answers.

Here we share the result of these efforts in an addendum to our September 2020 Final Report. In particular, this update focuses on whether the virus may have leaked from a medical research laboratory in Wuhan, Hubei Province, PRC, and the efforts to conceal such a leak. The evidence used to inform this report is based upon open source information and includes published academic work, official PRC publications (both public and confidential), interviews, emails, and social media postings.

Since the publication of the September 21, 2020 Final Report new questions have been raised pertaining to the origins of COVID-19. The PRC's continued lack of transparency resulted in President Joseph R. Biden, Jr.'s May 26, 2021, order to the United States Intelligence Community to prepare a report in 90 days on the origins of COVID-19, "including whether it emerged from human contact with an infected animal or from a laboratory accident." [1]

[1] "Statement by President Joe Biden on the Investigation into the Origins of COVID-19." The White House, 26 May 2021, www.whitehouse.gov/briefing-room/statements-releases/2021/05/26/statement-by-president-joe-biden-on-the-investigation-into-the-origins-of-covid-19/.

INTRODUCTION

Based on the material collected and analyzed by the Committee Minority Staff, the preponderance of evidence suggests SARS-CoV-2 was accidentally released from a Wuhan Institute of Virology laboratory sometime prior to September 12, 2019. The virus, or the viral sequence that was genetically manipulated, was likely collected in a cave in Yunnan province, PRC, between 2012 and 2015. Researchers at the WIV, officials within the CCP, and potentially American citizens directly engaged in efforts to obfuscate information related to the origins of the virus and to suppress public debate of a possible lab leak. It is incumbent on these parties to respond to the issues raised herein and provide clarity and any exonerating evidence as soon as possible. Until that time, it must be assumed General Secretary Xi and the Chinese Communist Party, prioritizes preserving the Party over the lives of its own people and those around the global suffering the effects of the COVID-19 pandemic.

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More than one year after the World Health Organization declared a pandemic, the world is still reeling from the emergence of the SARS-CoV-2 virus and the disease it causes, COVID-19. More than four million people have lost their lives worldwide, including more than 612,000 Americans, while economies around the world have been devastated by the fallout. This report investigates the origin of this virus and looks at how it became a deadly pandemic.

The Wuhan Institute of Virology

Last September, the House Foreign Affairs Committee Minority Staff, under the direction of Ranking Member Michael T. McCaul, released a report on the origins of the COVID-19 pandemic. That report highlighted the possibility SARS-CoV-2 could have leaked from the Wuhan Institute of Virology (WIV). However, as we continued our investigation and uncovered more information, we now believe it's time to completely dismiss the wet market as the source of the outbreak. We also believe the preponderance of the evidence proves the virus did leak from the WIV and that it did so sometime before September 12, 2019.

This is based upon multiple pieces of evidence laid out in the report, including:

- The sudden removal of the WIV's virus and sample database in the middle of the night on September 12, 2019 and without explanation;
- Safety concerns expressed by top PRC scientists in 2019 and unusually scheduled maintenance at the WIV;
- Athletes at the Military World Games held in Wuhan in October 2019 who became sick with symptoms similar to COVID-19 both while in Wuhan and also shortly after returning to their home countries;
- Satellite imagery of Wuhan in September and October 2019 that showed a significant uptick in the number of people at local hospitals surrounding the WIV's headquarters, coupled with an unusually high number of patients with symptoms similar to COVID-19;
- The installation of a People's Liberation Army's bioweapons expert as the head of the WIV's Biosafety Level 4 lab (BSL-4), possibly as early as late 2019; and
- Actions by the Chinese Communist Party and scientists working at or affiliated with the WIV to hide or coverup the type of research being conducted at there.

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Genetic Modification

This report also lays out ample evidence that researchers at the WIV, in conjunction with U.S. scientists and funded by both the PRC government and the U.S. government, were conducting gain-of-function research on coronaviruses at the WIV, at times under BSL-2 conditions. Much of this research was focused on modifying the spike protein of coronaviruses that could not infect humans so they could bind to human immune systems. The stated purpose of this work was to identified viruses with pandemic potential and to create a broad-spectrum coronavirus vaccine. In many instances, the scientists were successful in creating "chimeric viruses" – or viruses created from the pieces of other viruses – that could infect human immune systems. With dangerous research like this conducted at safety levels similar to a dentist's office, a natural or genetically modified virus could have easily escaped the lab and infected the community.

Committee Minority Staff has also identified scientists who are directly tied to the WIV, and who worked on gain-of-function research in the years prior to the start of the current pandemic, who had the ability to modify genetically modify coronaviruses without leaving any trace evidence. An American scientist, Dr. Ralph Baric, assisted in creating a method to leave no trace of genetic modification as early as 2005. And as early as 2016, scientists working at the WIV were able to do the same. This makes it clear that claims by the scientific community that SARS-CoV-2 could not be man-made because it has no genetic modification markers are disingenuous.

We conclude there is ample proof that the virus could have been genetically manipulated, and that it is vitally important we fully investigate this hypothesis to determine if that happened here.

The Cover-Up

In the original report, we laid out many of the ways the Chinese Communist Party (CCP) and the World Health Organization (WHO) went to great lengths to cover up the initial epidemic, and how their cover-up likely turned what could have been a local outbreak into a global pandemic. The CCP detained doctors in order to silence them, and disappeared journalists who attempted to expose the truth. They destroyed lab samples, and hid the fact there was clear evidence of human-to-human transmission. And they still refuse to allow a real investigation into the origins. At the same time, the WHO, under Director General Tedros, failed to warn the world of the impending pandemic. Instead, he parroted CCP talking points, acting as a puppet of General Secretary Xi.

In this addendum, we have uncovered further evidence of how top scientists at the WIV and Dr. Peter Daszak, an American scientist, furthered that cover-up. Their actions include bullying other scientists who questioned whether the virus could have leaked from a lab; misleading the world about how a virus can be modified without leaving a trace; and, in many, instances directly lying about the nature of the research they were conducting, as well as the low-level safety protocols they were using for that research.

These actions not only delayed an initial investigation into the possibility of a lab leak costing valuable time, but provide further proof the virus likely leaked from the WIV. These actions also call into question the way in which U.S. government grants are used in overseas labs and call for more oversight of those grants.

Next Steps

After this extensive investigation, we believe it is time to call Peter Daszak to testify before Congress. There are still many outstanding questions about the type of research he funded at the WIV that only he can answer. In addition, we believe there is legislation Congress can pass that would not only hold those responsible accountable but also help to prevent a future pandemic, including but not limited to:

- Institute a ban on conducting and funding any work that includes gain-of-function research until an international and legally binding standard is set, and only where that standard is verifiably being followed.
- Sanction the Chinese Academy of Sciences and affiliated entities.
- List the Wuhan Institute of Virology and its leadership on the Specially Designated Nationals and Blocked Persons List and apply additional, appropriate secondary sanctions.
- Authorize new sanctions for academic, governmental, and military bioresearch facilities that fail to ensure the appropriate levels of safety and information sharing.

GLOSSARY OF TERMS

Gain-of-Function Research	"Research that improves the ability of a pathogen to cause disease." – U.S. Department of Health and Human Services
Spike Protein	A protein structure on the surface of an enveloped virus responsible for anchoring the virus to the host cell's surface and enabling the injection of the virus' genetic material into the host cell.
RBD	Receptor-Binding Domain. The specific short fragment in a spike protein of a virus that binds the virus to a specific receptor on the host cell.
Primary Author	The first listed author of an academic paper, usually the person who contributes the most to a paper.
Corresponding Author	The point of contact for editors and outside readers who have questions about an academic paper.
USAID Predict	An epidemiological research grant program funded by the United States Agency for International Development. PREDICT provided funding for biological sampling aimed at virus identification and collection. The program provided grant funding to EcoHealth Alliance.
SARS	Severe Acute Respiratory Syndrome. A viral respiratory disease caused by SARS-CoV, a betacoronavirus. First identified as the cause of a 2002-2003 epidemic.
MERS	Middle East Respiratory Syndrome. A viral respiratory disease caused by MERS-CoV, a betacoronavirus. First identified as the cause of a 2012 outbreak.
SARS-CoV-2	The betacoronavirus that causes COVID-19.
Coronavirus	An RNA virus that causes disease in mammals and birds. Range in severity from the common cold to SARS-CoV-2.
Betacoronavirus	One of the four subclassifications of coronaviruses. Found in bats and rodents, this is the genus includes SARS, MERS, and SARS-CoV-2.
Biosafety Level 1 (BSL1)	Designed for work on microbes not known to cause disease in healthy adults and present minimal potential hazard to laboratorians and the environment. Work can be performed on an open lab bench or table.

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Biosafety Level 2 (BSL2)	For work with microbes that pose moderate hazards to laboratorians and the environment. The microbes are typically indigenous and associated with diseases of varying severity. Personal protective equipment includes lab coats and gloves. Work can be performed in the open or in a biological safety cabinet. Commonly compared to the level of safety observed in a dentist’s office.
Bio Safety Level 3 (BSL3)	For work with microbes that are either indigenous or exotic, and that can cause serious or potentially lethal disease through respiratory transmission. Respiratory transmission is the inhalation route of exposure. Researchers should be under medical surveillance and potentially immunized for the microbes they work with. Respirators may be required, in addition to standard personal protective equipment. Work must be performed within a biological safety cabinet. Exhaust air cannot be recirculated, and the laboratory must have sustained directional airflow by drawing air into the laboratory from clean areas towards potentially contaminated areas.
Biosafety Level 4 (BSL4)	This is the highest level of biological safety. The microbes in a BSL-4 lab are dangerous and exotic, posing a high risk of aerosol-transmitted infections. Infections caused by these microbes are frequently fatal and without treatment or vaccines. Researchers must change clothing prior to entering the lab, shower upon exiting, and decontaminate all materials before exiting. All work with microbes must be performed in a Class III biological safety cabinet or while wearing a full body, air-supplied, positive pressure suit. The lab must be in a separate building or in a restricted zone, and must have a dedicated supply and exhaust air, as well as vacuum lines and decontamination systems.
Wuhan Institute of Virology (WIV)	A research institute in Wuhan, PRC focused on focused on virology, that consists of at least two facilities – the Wuhan National Biosafety Laboratory and the Wuhan Institute of Virology Headquarters.”

GLOSSARY OF TERMS

Wuhan National Biosafety Laboratory	The WIV's new campus, located in the Zhengdian Scientific Park in Jiangxia District, Wuhan. The location of the WIV's Biosafety Level 4 laboratory space.
WIV Headquarters	The older WIV facility, located in Wuchang District, Wuhan near the Wuhan Branch of the Chinese Academies of Science.
Chinese Academy of Sciences	The national academy for natural sciences in the PRC. Reports to the State Council of the People's Republic of China.
WIV1	The first novel coronavirus isolated by WIV researchers. Isolated from bat fecal samples in 2013. A SARS like coronavirus.
WIV16	The second coronavirus isolated by WIV researchers. Isolated from a single bat fecal sample in 2016. A SARS like coronavirus.
Rs4874	The third coronavirus isolated by WIV researchers. Isolated from a single bat fecal sample in 2017. A SARS like coronavirus.
ID4491/RaTG13	A SARS like coronavirus collected in 2013 in a mining cave. 96.1% similar to SARS-CoV-2.
ACE2	Angiotensin-converting enzyme-2, found on the surface of certain cells in a variety of animals, including humans, mice, and civets. The entry point for coronaviruses.
hACE2	The human version of ACE2. Primarily found on the surface of cells and tissues throughout the human body, including the nose, mouth, and lungs. In the lungs, hACE2 is highly abundant on type 2 pneumocytes, an important cell type present in chambers within the lung called alveoli, where oxygen is absorbed, and waste carbon dioxide is released. The primary entry point for SARS-CoV-2 into human cells.
Chimeric Virus	An artificial, man-made virus. Created by joining two or more viral fragments.
Natural Virus	A virus found in nature; "wild type."

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Reverse Genetics System	A method in molecular genetics that is used to help understand the function(s) of a gene by analyzing the phenotypic effects caused by genetically engineering specific nucleic acid sequences within the gene. Can be used to create chimeric viruses indistinguishable from natural viruses.
Furin Cleavage Site	An enzyme in the spike protein of SARS-CoV-2 that increases how infectious the virus is in humans. SARS-CoV-2 is the only betacoronavirus to have this structure.
Phylogenetic Analysis	The study of the evolutionary development of a species or a group of organisms or a particular characteristic of an organism. Used to identify the relationship between different viruses in the same family.
CGG Double Codon	"CGG-CGG." This group of six nucleotides (a group of three nucleotides is also know as a codon) is half of the 12 nucleotides that create the furin cleavage site. The CGG double codon is relatively rare in coronaviruses, and SARS-CoV-2 is the only coronavirus in its family to have one.

KEY PEOPLE

Dr. Wang Yanyi	Director General of the Wuhan Institute of Virology.
Dr. Yuan Zhiming	Director of the WNBL BSL-4 lab. General Secretary of the Chinese Communist Party Committee within the Wuhan Branch of the Chinese Academy of Sciences, to which the WIV belongs.
Dr. Shi Zheng-li	Senior scientist as the Wuhan Institute of Virology (WIV). Serves as Director, Research Center for Emerging Infectious Diseases; Director, Chinese Academy of Sciences Key Laboratory of Special Pathogens; Director, Biosafety Working Committee; and Deputy Director of the Wuhan National Biosafety Laboratory's Biosafety-Level 4 lab.
Dr. Ben Hu	WIV researcher and former doctoral student of Shi Zheng-li. Deeply involved in the WIV's coronavirus research.
Dr. Linfa Wang	PRC national, Director and Professor of the Program in Emerging Infectious Diseases at the Duke-NUS Graduate Medical School in Singapore. Chair of the Scientific Advisory Board for the Center for Emerging Diseases at the WIV.
Dr. Peter Daszak	CEO of EcoHealth Alliance. Longtime collaborator of Shi and others at the WIV. Provided subgrants to the WIV to help fund coronavirus research.
Dr. Ralph Baric	Researcher at the University of North Carolina at Chapel Hill who has collaborated with Shi and other WIV researchers on coronavirus research.

ADDENDUM TO THE REPORT

I. THE CITY OF WUHAN: EPICENTER OF A PANDEMIC

Wuhan is the epicenter of the coronavirus pandemic. Located in central PRC where the Yangtze River, the PRC's longest river, and the Han River meet, Wuhan is the capital city of Hubei Province and boasts a population of about 11.1 million in about 3,280 square miles. [2] It is home to the PRC's tallest skyscrapers, multiple colleges and universities, including the prominent Wuhan University, major historical and cultural sites, and an influential research laboratory, the Wuhan Institute of Virology (WIV). To put the scale of Wuhan in perspective, the city covers an area five times the size of Houston and has a larger population than New York City and Chicago combined.

Wuhan is home to the Hankou railway station, central PRC's biggest European-style Railway station, and two other major train stations. Hankou Station connects directly to the Tianhe International Airport, the busiest airport in central PRC and the geographic center of the PRC's airport network. From the Tianhe airport, travelers can fly direct to New York City, San Francisco, Paris, Milan, Rome, Hamburg, Bangkok, Tokyo, Seoul, and Dubai, among many other destinations around the world.

The PRC calls Wuhan one of its nine "National Central Cities," an official state label that means it leads the way, along with the capital Beijing, Shanghai, and other major cities, in developing culture, politics, and the economy.[3] An August 2016 report by the Netherlands Enterprise Agency, a government agency that operates under the auspices of the Ministry of Economic Affairs and Climate Policy, identified Wuhan as a major hub not just within the PRC, but also globally within the Chinese "One Belt One Road" initiative due to its accessibility.[4] The city is also home to significant railway commerce. A 2018 report from Xinhua news expected an estimated 500 freight trains from Wuhan to Europe for the export of goods.[5]

France, the U.S., the Republic of Korea, and the UK maintain Consulates in the city, which was selected to host the 7th International Military Sports Council (CISM) Military World Games. During the games, more than 9,000 military personnel from over 100 countries stayed in Wuhan in accommodations at an athletes' village built specifically for the games.

2 "WHO-convened Global Study of Origins of SARS-CoV-2: China Part." Joint WHO-China Study. 30 March 2021, https://www.who.int/health-topics/coronavirus/origins-of-the-virus

3 Xu, Zongwei. "China Unveils National Central City Strategy." *China Watch,* 29 Mar. 2018, www.chinawatch.cn/a/201803/29/WS5ad061d6a310cc9200067c6c.html.

4 Van de Bovenkamp, Judith and Yuan Fei. "Economic Overview of Hubei Province." *Neatherlands Business Support Office Wuhan,* Aug. 2016, https://www.rvo.nl/sites/default/files/2016/08/Economic-overview-Hubei-province-China.pdf

5 "Central China-Europe Rail Freight to Surge in 2018." *Xinhua*, 1 Feb. 2018. http://www.china.org.cn/china/Off_the_Wire/2018-02/01/content_50372222.htm

II. EVIDENCE OF A LAB LEAK

As discussed in the previously issued report, the WIV continues to be a focal point of debate concerning the origins of SARS-CoV-2 and the COVID-19 pandemic. In recent months, new information about the WIV has come to light, enabling us to better understand the institute, the type of research conducted by scientists working there, and its ties to the CCP and their military, the People's Liberation Army (PLA). We now believe the preponderance of evidence shows the virus accidentally leaked from one of the WIV's facilities.

The Wuhan Institute of Virology

The WIV was founded in 1956 as the Wuhan Microbiology Laboratory and has operated under the administration of the Chinese Academy of Sciences since 1978.[6] The institute currently occupies at least two campuses – the much-discussed Wuhan National Biosafety Laboratory (WNBL) in Zhengdian Scientific Park (see Figure 1), and the older facility (hereafter WIV Headquarters) located in the Xiaohongshan park in the Wuchang District of Wuhan (see Figure 2). The WNBL is a large complex with multiple buildings that house 20 Biosafety Level II (BSL-2) laboratories, two Biosafety Level III (BSL-3) laboratories, and 3000 square meters of Biosafety Level IV (BSL-4) space, "including four independent laboratories areas and two animal suites."[7] Construction was completed in 2015, but due to delays the BSL-4 space did not become operational until early 2018.[8]



Fig. 1: Wuhan National Biosafety Laboratory (WNBL)

Missing from the majority of public debates regarding the WIV is the research conducted at the WIV Headquarters, the older location in the Wuchang District of Wuhan. Located 12 miles northeast of the WNBL, in the Wuchang District, this facility remains the administrative headquarters of the WIV. In addition to the BSL-2 labs at this location, the WIV constructed a BSL-3 laboratory at the facility in 2003.[9]

6 "History." *Wuhan Institute of Virology*, http://english.whiov.cas.cn/About_Us2016/History2016/.

7 World Health Organization. "WHO Consultative Meeting on High/Maximum Containment (Biosafety Level 4) Laboratories Networking." Meeting Report, Lyon, France, 13-15 Dec. 2018. https://apps.who.int/iris/bitstream/handle/10665/311625/WHO-WHE-CPI-2018.40-eng.pdf

8 Zhiming, Yuan. "Current status and future challenges of high-level biosafety laboratories in China." *Journal of Biosafety and Biosecurity,* 1 Sept. 2019, 1(2): 123-127. https://doi.org/10.1016/j.jobb.2019.09.005

9 Zheng Qianli, "Jiang Xia plays new essays and plays Yoko on the crane——The construction and research team of P4 laboratory of Wuhan Institute of Virology, Chinese Academy of Sciences." *Chinese Journal of Science,* 1 Jan. 2018, https://archive.is/V3GHk#selection-517.35-517.202

It was here, in the center of Wuhan, that Dr. Shi Zheng-li and her team conducted gain-of-function research on coronaviruses in the years leading up to the COVID-19 pandemic.



Fig. 2: WIV Headquarters in Wuchang

According to the WIV's website, Shi Zheng-li serves as the Director of the WIV's Research Center for Emerging Infectious Diseases, the Deputy Director of the WNBL BSL-4 lab, the Director of the BSL-3 lab, and the Director of the Biosafety Working Committee.[10] Shi is also the Director of the Chinese Academy of Sciences (CAS) Key Laboratory of Special Pathogens and Biosafety,[11] which includes the majority of scientists who are conducting gain-of-function research on coronaviruses at the WIV.

It should be noted that the WIV has a Chinese Communist Party Committee within the institute, as well as a Commission for Discipline Inspection. The Party Committee is divided into four party branches, which are then divided into subbranches organized around the individual WIV departments, research centers, and offices. Each subbranch has its own Propaganda Committee. Committee Minority Staff were able to identify eight WIV researchers on these committees, including several who are affiliated with the Key Laboratory that Shi directs.

WIV Researcher	Lab Affiliation	Propaganda Committee[12]
Liu Qiaojiue	Key Laboratory of Special Pathogens and Biosafety[13]	Party Branch of Research Center for Emerging Infectious Diseases
Zhang Xiaowei	Key Laboratory of Special Pathogens and Biosafety and Key Laboratory of Virology[14]	Party Branch of the Research Center for Microbiology and Nanobiology

10 "Shi Zhingli." Wuhan Institute of Virology, http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100074.html

11 "Prof. SHI Zhengli elected a fellow of the American Academy of Microbiology." *Wuhan Institute of Virology,* http://english.whiov.cas.cn/ne/201903/t20190308_206697.html

12 "Party Branch." Wuhan Institute of Virology, http://www.whiov.cas.cn/djkxwh/dqzz/dzb/

13 Wang Q, et. al. "Structural Basis for RNA Replication by the SARS-CoV-2 Polymerase." *Cell,* 23 July 2020, 182(2):417-428.e13, https://pubmed.ncbi.nlm.nih.gov/32526208/

14 Zhang, Xiaowei et al. "Tick-borne encephalitis virus induces chemokine RANTES expression via activation of IRF-3 pathway." *Journal of Neuroinflammation,* 30 Aug. 2016, 13(1):209. https://pubmed.ncbi.nlm.nih.gov/27576490/

Shen Xurui	Key Laboratory of Special Pathogens and Biosafety [15]	Graduate Party Branch of the Research Center for Emerging Infectious Diseases
Tang Shuang	State Key Laboratory of Virology [16]	Party Branch of the Research Center for Microbial Resources and Bioinformatics
Wu Yan	State Key Laboratory of Virology [17]	Party Branch of Molecular Virus and Pathology Research Center
He Lihong	State Key Laboratory of Virology [18]	Party Branch of the Research Center for Microbial Resources and Bioinformatics
Wang Qingxing	State Key Laboratory of Virology [19]	Graduate Party Branch of the Research Center for Molecular Viruses and Pathology
Yang Mengsi	State Key Laboratory of Virology [20]	Graduate Party Branch of the Research Center of Microbiology and Nanobiology

Table 1: WIV Researchers on CCP Propaganda Committees

The Committee for Discipline Inspection is charged with "the implementation of the party's line, policy, party discipline, relevant laws and regulations, and the institute's rules and regulations."[21]

In addition to the researchers serving on propaganda committees, other key figures at the WIV also serve as CCP officials. Dr. Wang Yanyi serves as the Director of the WIV and joined the China Zhi Gong Party, a CCP controlled minority party, in 2010. In 2018, the same year she became the Director General of the WIV, she was elected the Deputy Director of the Wuhan Municipal Party Committee.

15 Zhou, Peng et al. "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature* March 2020, 579(7798): 270-273. https://pubmed.ncbi.nlm.nih.gov/32015507/

16 Abudurexiti, Abulikemu, et al. "Taxonomy of the order Bunyavirales: update 2019." *Archives of Virology,* July 2019, 164(7): 1949-1965. https://pubmed.ncbi.nlm.nih.gov/31065850/

17 Su, Hai-Xia et al. "Anti-SARS-CoV-2 activities in vitro of Shuanghuanglian preparations and bioactive ingredients." *Acta Pharmacologica Sinica,* September 2020, 41(9): 1167-1177. https://pubmed.ncbi.nlm.nih.gov/32737471/

18 Shao, Wei et al. "Functional Characterization of the Group I Alphabaculovirus Specific Gene ac73." *Virologica Sinica,* Dec. 2019, 34(6): 701-711. https://pubmed.ncbi.nlm.nih.gov/31317397/

19 Su, Haixia et al. "Identification of pyrogallol as a warhead in design of covalent inhibitors for the SARS-CoV-2 3CL protease." *Nature Communications,* 15 June 2021, (2(1): 3623. https://pubmed.ncbi.nlm.nih.gov/34131140/

20 Zhang, Juan, et. al. "Passive cancer targeting with a viral nanoparticle depends on the stage of tumorigenesis." *Nanoscale*, 8 July 2021, 13(26):11334-11342, https://pubmed.ncbi.nlm.nih.gov/34165123/

21 "Commission for Discipline Inspection." *Wuhan Institute of Virology,* http://www.whiov.cas.cn/djkxwh/dqzz/jw/

Until late 2019, the BSL-4 lab was managed by Dr. Yuan Zhiming. Yuan is the General Secretary of the Chinese Communist Party Committee within the Wuhan Branch of the Chinese Academy of Sciences, to which the WIV belongs. Local CCP leaders not only run the WIV itself but also directly managed the BSL-4 lab.[22]

Director Wang's 2021 New Year's speech makes reference to the Party Committee of Wuhan Institute of Virology, pledging that the party committee will "effectively play the role of a battle fortress of grassroots party organizations."[23] The WNBL also has its own party branch, the Zhengdian Laboratory Party Branch, which was "awarded the title of 'Red Flag Party Branch' by the Hubei Provincial Party Committee and Provincial Organization Working Committee, effectively playing an advanced and exemplary role."[24] Notably, in discussing the COVID-19 pandemic, Director Wang's 2021 speech takes pains to address questions of lab safety – "The institute's high-level biosafety laboratory operates safely for more than 300 days throughout the year."[25] Her 2020 address, posted sometime after April 2020, makes no such mention.

The WNBL's BSL-4 lab was constructed as a result of an agreement between the PRC and France that was signed after the 2003 SARS pandemic.[26] At the time, all BSL-3 labs in the PRC were controlled by the PRC's People's Liberation Army (PLA). Then-President of France, Jacques Chirac, and his Prime Minister, Jean-Pierre Raffarin, approved the project despite concerns from both the French Ministry of Defense and French intelligence services – Raffarin himself described it as "a political agreement."[27] The PRC was suspected of having a biological warfare program, and the military and intelligence services were worried that the dual-use technology required to build a BSL-4 lab could be misused by the PRC government. The uneasy compromise reached within the French government was that the agreement would require joint PRC-France research to be conducted in the lab, with French researchers present.[28]

In 2016, the PRC requested dozens of the containment suits required to work in the lab. The French Dual-Use Commission, tasked with considering exports of sensitive equipment, rejected their request. According to French reporting, the request was "well above the needs of the Wuhan [lab]."[29] **This continued to fuel concerns within the French Ministry of Defense that the PRC was seeking to engage in military research or open a second BSL-4 lab for military means.** Despite the agreement that the BSL-4 lab would be a site of joint research, and an announcement at the 2017 inauguration by then Prime Minister Bernard Cazeneuve of €5 million in funding, there has only been one French scientist assigned to the lab. His tour ended in 2020.[30]

22 Izambard, Antoine. "L'histoire Secrète Du Laboratoire P4 De Wuhan Vendu Par La France à La Chine." *Challenges,* 30 Apr. 2020 www.challenges.fr/entreprise/sante-et-pharmacie/revelations-l-histoire-secrete-du-laboratoire-p4-de-wuhan-vendu-par-la-france-a-la-chine_707425.

23 "New Year's Speech by the Director in 2021." *Wuhan Institute of Virology,* http://www.whiov.cas.cn/gkjj/szzc_160220/

24 "New Year's Message from the Director in 2020." *Wuhan Institute of Virology,* https://web.archive.org/web/20200701032318/http://www.whiov.cas.cn/gkjj/szzc_160220/

25 *Ibid.*

26 "About WIV." *Wuhan Institute of Virology,* http://english.whiov.cas.cn/About_Us2016/Brief_Introduction2016/.

27 Izambard, Antoine. "L'histoire Secrète Du Laboratoire P4 De Wuhan Vendu Par La France à La Chine." *Challenges*, 30 Apr. 2020, www.challenges.fr/entreprise/sante-et-pharmacie/revelations-l-histoire-secrete-du-laboratoire-p4-de-wuhan-vendu-par-la-france-a-la-chine_707425.

28 *Ibid.*

29 *Ibid.*

30 Izambard.

Safety Concerns and Unusual Maintenance

There have been several reports of safety concerns at PRC labs starting as early as 2004, when it was discovered SARS leaked from a lab in Beijing. Several other accidental releases have happened in the years since.

As discussed in our original report released last year, in 2018 U.S. State Department officials sent cables to Washington, D.C. highlighting concerns with safety issues at the WIV. The cables reported that scientists at the WIV noted "a serious shortage of appropriately trained technicians and investigators needed to safely operate this high-containment laboratory."[31] The cables also questioned the PRC's commitment to prioritizing the important research for which the lab was designed.

> (b)(6) Thus, while the BSL-4 lab is ostensibly fully accredited, its utilization is limited by lack of access to specific organisms and by opaque government review and approval processes. As long as this situation continues, Beijing's commitment to prioritizing infectious disease control - on the regional and international level, especially in relation to highly pathogenic viruses, remains in doubt.

Fig. 4: Excerpt from January 19, 2018 Cable from the U.S. Embassy in Beijing to State Department Headquarters in Washington, D.C.

One year later, in June 2019, George Gao, the Director of the Chinese Center for Disease Control and Prevention, expressed concerns about safety protocols at the WIV. In an almost prophetic statement published in *Biosafety and Health*, Gao wrote (emphasis added):

> Advances in biomedical technologies, such as genome editing and synthetic biotechnology, have the potential to provide new avenues for biological intervention in human diseases. These advances may also have a positive impact by allowing us to address risks in new approaches. **However, the proliferation of such technologies means they will also be available to the ambitious, careless, inept, and outright malcontents, who may misuse them in ways that endanger our safety.** For example, while CRISPR-related techniques provide revolutionary solutions for targeted cellular genome editing, it can also lead to unexpected off-target mutations within genomes or the possibility of gene drive initiation in humans, animals, insects, and plants. Similarly, genetic modification of pathogens, which may expand host range as well as increase transmission and virulence, may result in new risks for epidemics. For example, in 2013, several groups showed that influenza H5N1 viruses with a few nucleotide mutations and H7N9 isolates reasserted with 2009 pandemic H1N1 virus could have the ability for airborne transmission between ferrets. **Likewise, synthetic bat-origin SARS-like coronaviruses acquired an increased capability to infect human cells. Thus, modifying the genomes of animals (including humans), plants, and microbes (including pathogens) must be highly regulated.**[32]

Three months later, in September 2019, Yuan Zhiming, the Director of the BSL-4 lab at the WNBL and Shi's superior, published an article in the *Journal of Biosafety and Biosecurity.*

31 Rogin, Josh. "Opinion | State Department Cables Warned of Safety Issues at Wuhan Lab Studying Bat Coronaviruses." *The Washington Post,* 14 Apr. 2020, www.washingtonpost.com/opinions/2020/04/14/state-department-cables-warned-safety-issues-wuhan-lab-studying-bat-coronaviruses/.

32 Gao, George F. "For a better world: Biosafety strategies to protect global health." *Biosafety and Health,* June 2019, 1(1): 1-3. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7147920/

Entitled, "Current status and future challenges of high-level biosafety laboratories in China,"[33] the article discusses at length the construction of the WNBL. Yuan identifies multiple key issues, including inadequate biosafety management systems, insufficient resources for efficient laboratory operation, and deficiency of professional capacity. With a surprising level of transparency, Yuan admits that the enforcement of pathogen, waste, and laboratory animal management regulations "needs to be strengthened."[34] Discussing the insufficient level of resources being provided by the PRC government, he stated:

> **The maintenance cost is generally neglected; several high-level BSLs have insufficient operational funds for routine yet vital processes. Due to the limited resources, some BSL-3 laboratories run on extremely minimal operational costs or in some cases none at all.**[35]

Yuan also raised concerns about a lack of specialized biosafety managers and engineers to run the labs.[36] **It is important to note that researchers at the WIV had previously conducted gain-of-function research on coronaviruses at the BSL-2 and BSL-3 levels. This is important given that both the head of the China CDC and the head of the WIV's BSL-4 labs had expressed concern about the safety of this research and the labs in which it was being conducted.**

Interestingly, there appears to have been ongoing maintenance and repairs projects occurring at the WIV in 2019, before Yuan published his article raising these concerns. It is important to note that at the time of the hazardous waste treatment system renovation project, the WNBL had been operational for less than two years. Such a significant renovation so soon after the facility began operation appears unusual. Procurement announcements published on the PRC's government procurement website provide evidence of ongoing work at what appears to be both WIV locations.

Project Name	Location	Date	Budget (USD)
Maintenance Project of P3 Laboratory and Laboratory Animal Center in Zhengdian Park[37]	WNBL	March 1, 2019	$401,284.10
Procurement of Positive Pressure Protective Clothing[38]	WNBL	March 21, 2019	$177,161.40
Hazardous Waste Treatment System Renovation Project[39]	WNBL	July 31, 2019	$1,521,279.28

33Yuan Zhinming. "Current status and future challenges of high-level biosafety laboratories in China." *Journal of Biosafety and Biosecurity,* Sept. 2019, 1(2): 123-127. https://www.sciencedirect.com/science/article/pii/S2588933819300391#b0080

34*Ibid.*

35*Ibid.*

36*Ibid.*

37"Announcement of Competitive Consultation on Maintenance Project of P3 Laboratory and Laboratory Animal Center in Zhengdian Park, Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network,* 1 March 2019, https://archive.is/7eCPU#selection-229.0-229.185

38"Announcement of a single source for the purchase of positive pressure protective clothing project by Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network,* 21 March 2019, https://archive.is/VUcNA#selection-229.0-229.157

39"Announcement on the transaction of the hazardous waste treatment system renovation project in Zhengdian Park, Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network,* 31 July 2019, https://archive.is/3CW03#selection-229.0-229.166

Procurement Project of The Environmental Air Disinfection System and The Scalable Automated Sample Storage Management System [40]	Unclear	August 14, 2019	$132,200,025.47
Security Service Procurement Project [41]	WNBL	September 12, 2019	$1,281,022.33
Central Air Conditioning Renovation Project [42]	Unclear	September 16, 2019	$606,382,986.11
Procurement of Air Incinerator and Testing Service [43]	Unclear	December 3, 2019	$49,388.81

Table 2: WIV Procurement Projects in 2019

The references to maintenance at the BSL-3 and animal center at the WNBL, the procurement of an environmental air disinfection system, and renovations to the hazardous waste treatment system and central air conditioning system all raise questions about how well these systems were functioning in the months prior to the outbreak of COVID-19.

The Disappearing Database

On September 12, 2019 the WIV's online, public database of samples and virus sequences was taken offline in the middle of the night between 2:00AM and 3:00AM local time.[44] The database contained more than 22,000 entries consisting of sample and pathogen data collected from bats and mice. The database contained key information about each sample, including what type of animal it was collected from, where it was collected, whether the virus was successfully isolated, the type of virus collected, and its similarity to other known viruses.

40 "Announcement of winning the bid for the procurement project of the environmental air disinfection system and the scalable automated sample storage management system of the Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network,* 14 Aug. 2019, https://archive.is/1nXLD#selection-229.0-229.228

41 "Competitive consultation on the procurement project of security services in Zhengdian Science Park, *Wuhan Institute of Virology,* Chinese Academy of Sciences." *China Government Procurement Network, 12* Sept. 2019,https://archive.is/tUi75#selection-229.0-229.156

42 "Competitive Consultation on Central Air Conditioning Renovation Project of Wuhan Institute of Virology, Chinese Academy of Sciences." *China Government Procurement Network,* 16 Sept. 2019, https://archive.is/bfoTD#selection-229.0-229.131

43 "The Wuhan Institute of Virology of the Chinese Academy of Sciences plans to use a single-source procurement method to publicize the procurement of air incineration devices and test service projects." *China Government Procurement Network,* 3 Dec. 2019, https://archive.is/Jifqr#selection-229.0-229.197

44 "Status breakdown of the database of characteristic wild animals carrying virus pathogens (September 2019)." *Scientific Database Service Monitoring & Statistics System.* https://archive.is/AGtFv#selection-1553.0-1567.2

Table 1 Virus data display of bat samples

Data element name	Example
Sample ID	162387A
Sample tissue type	Anal
Animal type	bat
Source species	*Rousettus leschenaultii*
Species molecular identification	*Rousettus* sp.
Collection date	2016-08-21
country	China
province	Yunnan
city	Miaoxin village, Mengna county, Sipsongpanna
GPS information	101.51944,21.78127
Whether high-throughput sequencing	No
Whether the virus is isolated	No
publishing	Luo Y, Li B, Jiang RD, et al. *Virol Sin*. 2018;33(1):87–95. doi:10.1007/s12250-018-0017-2
Remarks	
Detection method	PCR-based
Virus name	Coronaviridae
Test results	Positive
blast result	btcov HKU9
Virus classification	HKU9
Virus sequence	See references for details
Similarity	94%
Sequence length	398bp
Sequence-encoded gene	Partial RdRp

Fig. 6: Example Database Entry [45]

To date, there has been no consistent answer provided as to why the database was removed or when or if it will be put back online.

Shi is listed as the data correspondence author for the project. When questioned about the database being taken offline, Shi has given several conflicting answers. During a December 2020 interview with *BBC*, Shi said the database was taken offline for "security reasons" after cyberattacks against the work and personal emails of WIV staff. She also insisted that WIV virus sequences were saved in the GenBank database, run by the National Center for Biotechnology Information. Shi stated, "It's completely transparent. We have nothing to hide." [46]

In a January 26, 2021 email to someone inquiring about the database, however, Shi stated the database was taken down due to cyberattacks "during [the] COVID-19 pandemic."[47] She also claimed that researchers had "only entered a limit[ed] data in this database" despite it having more than 22,000 entries.

45 "Database of pathogens of bat and murine viruses." *Wikisource*, https://zh.wikisource.org/zh-hant/%E8%9D%99%E8%9D%A0%E6%BA%90%E5%92%8C%E9%BC%A0%E6%BA%90%E7%97%85%E6%AF%92%E7%97%85%E5%8E%9F%E6%95%B0%E6%8D%AE%E5%BA%93

46 Sudworth, John. "Covid: Wuhan Scientist Would 'Welcome' Visit Probing Lab Leak Theory." *BBC News,* 21 Dec. 2020, www.bbc.com/news/world-asia-china-55364445.

47 Cleary, Tommy. "Prof Zheng-Li Shi Replied to Me, to CNRI,中文DOI运维 I Can Only Conclude @PeterDaszak & the Rest of the @WHO Organisation Were given the Same Information Access Ultimatum:No Trust, No Conversation.@SciDiplomacyUSA Has Its Work Cut Out.Data Hostage? Pic.twitter.com/KhiFs42U7j." *Twitter*, 10 Mar. 2021, https://twitter.com/tommy_cleary/status/1369689088790425602?s=20.

In an apparent contradiction of her *BBC* interview, Shi admitted that "access to the visitors is limited,"[48] but maintains:

> **…all our work regarding the different type of bat coronavirus (partial sequences or full-length genome sequences) have been published and the sequence and sample information have been submitted to GenBank.**[49]

At the end of her email, Shi writes, "I'll not answer any of your questions if your curiosity is based on the conspiracy of 'man made or lab leak of SARS-CoV-2' or some non-sense questions based on your suspicion. **No trust, no conversation**"[50] (emphasis added).

New Leadership and PLA Involvement

The WIV's website indicates that Yuan Zhiming serves as the Dean of the Wuhan Branch of the Chinese Academy of Sciences and director of the WNBL BSL-4 lab.[51] However, news posted on Weibo Douban, a PRC website, on February 7th, 2020 stated that PLA officials were dispatched to assume control of the response. **The report says PLA Major General Chen Wei, an expert in biology and chemical weapon defenses , was deployed to Wuhan in January 2020 and took control of the WNBL BSL-4 lab.** The posting of this information to Douban is significant given the website's history of censoring posts critical of the CCP, including censoring words related to the Tiananmen Square Massacre.[54] The post's survival on a heavily CCP censored site confirms its legitimacy.



48 Sudworth.

49 *Ibid.*

50 *Ibid.*

51 "Yuan Zhiming." *Wuhan Institute of Virology*, http://www.whiov.cas.cn/sourcedb_whiov_cas/zw/rck/200907/t20090718_2100080.html

52 Gertz, Bill. "Chinese Maj. Gen. Chen Wei TAKES Leading Role in Coronavirus Fight." *The Washington Times,* 16 Feb. 2020, www.washingtontimes.com/news/2020/feb/16/chinese-maj-gen-chen-wei-takes-leading-role-in-cor/.

53 Guli. "Major General Chen Wei, China's Chief Biochemical Weapons Expert, Takes Over Wuhan P4 Virus Laboratory." *Radio France Internationale,* https://www.rfi.fr/cn/%E4%B8%AD%E5%9B%BD/20200208-%E4%B8%AD%E5%9B%BD%E9%A6%96%E5%B8%AD%E7%94%9F%E5%8C%96%E6%AD%A6%E5%99%A8%E4%B8%93%E5%AE%B6%E9%99%88%E8%96%87%E5%B0%91%E5%B0%86%E6%8E%A5%E7%AE%A1%E6%AD%A6%E6%B1%89p4%E7%97%85%E6%AF%92%E5%AE%9E%E9%AA%8C%E5%AE%A4

54 Honorof, Marshall. "China Marks Tiananmen Massacre with 'Internet Maintenance Day.'" *NBC News,* 4 June 2013, https://www.nbcnews.com/id/wbna52096871

Committee Minority Staff have also received testimony from a former senior U.S. official that Gen. Chen actually took control of the WNBL BSL-4 lab in late 2019, not January 2020 as was publicly reported. Gen. Chen taking over part of the WIV demonstrates the CCP was concerned about the activity happening there as news of the virus was spreading. If she took control in 2019, it would mean the CCP knew about the virus earlier, and that the outbreak began earlier – a topic discussed further in this section.

Gen. Chen is a researcher at the Academy of Military Medical Sciences in Beijing, and served as a delegate to the 12th National People's Congress.[55] In January 2018, Gen. Chen was made a member of the 13th National Committee of the Chinese People's Political Consultative Conference (CPPCC). According to the U.S.-China Economic Security Review Commission, the CPPCC is a "critical coordinating body that brings together representatives of China's other interest groups and is led by a member of China's highest-level decision-making authority, the CCP's Politburo Standing Committee." [56]

According to a January 15, 2021 fact sheet published by the State Department, in the years leading up to the pandemic, researchers at the WIV were engaged in classified research, including experiments on animals, on behalf of the PLA.[57] Dr. Shi has repeatedly denied any involvement of the PLA at the WIV. During a lecture hosted only by Rutgers Medical School, Shi stated:

> We—our work, our research is open, and we have a lot of international collaboration. And from my knowledge, all our research work is open, is transparency. So, at the beginning of COVID-19, we heard the rumors that it's claimed in our laboratory we have some project, blah blah, with army, blah blah, these kinds of rumors. But this is not correct because I am the lab's director and responsible for research activity. I don't know any kind of research work performed in this lab. This is incorrect information.[58]

This statement is demonstrably false. The WIV had multiple connections to PLA researchers prior to the COVID-19 pandemic; several were listed on the WIV's English language website. The Academic Committee of State Key Laboratory of Virology at the WIV included a Deputy Director from the Second Military Medical University and a member from the 302 Military Hospital of China. The Scientific Advisory Committee for the Center for Emerging Infectious Diseases had among its members a researcher from the Institute of Military Veterinary at the Academy of Military Medical Sciences.[59] This website was scrubbed on May 28, 2020, and the lists of committee members removed. However, archived copies of the website are available online.

55 "List of Deputies to the Twelfth National People's Congress of the People's Republic of China." *Sohu,* http://news.sohu.com/20130227/n367313787.shtml

56 Bowe, Alexander. "China's Overseas United Front Work: Background and Implications for the United States." *U.S.-China Economic and Security Review Commission,* 24 Aug. 2018, https://www.uscc.gov/sites/default/files/Research/China%27s%20Overseas%20United%20Front%20Work%20-%20Background%20and%20Implications%20for%20US_final_0.pdf

57 United States, Department of State. "Fact Sheet: Activity at the Wuhan Institute of Virology." 15 Jan. 2021, https://2017-2021.state.gov/fact-sheet-activity-at-the-wuhan-institute-of-virology/index.html

58 Eban, Katherine. "The Lab-Leak Theory: Inside the Fight to Uncover COVID-19's Origins." *Vanity Fair,* 3 June 2021, www.vanityfair.com/news/2021/06/the-lab-leak-theory-inside-the-fight-to-uncover-covid-19s-origins.

59 "Committees." *Wuhan Institute of Virology,* https://web.archive.org/web/20200527045823/http://english.whiov.cas.cn/About_Us2016/Committees/

Academic Committee of State key laboratory of virology, WIV, CAS

Director: Zihe RAO, Tsinghua University, China.

Deputy Directors: Hongyang WANG, The Second Military Medical University, China.

Hongbin SHU, Wuhan University, China.

Members:

Jianfang GUI, Institute of Hydrobiology, Chinese Academy of Sciences, China.

Fusheng WANG, 302 Military Hospital of China, China.

Hualan CHEN, Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, China.

Zhenghong YUAN, Fudan University, China.

Ningshao XIA, Xiamen University, China.

Linqi ZHANG, Tsinghua University, China.

Musheng ZENG, Sun Yat-sen University, China.

Jianguo WU, Wuhan University, China.

Xinwen CHEN, Wuhan Institute of Virology, Chinese Academy of Sciences, China.

Ke LAN, Wuhan University, China.

Fig. 3: Archived Versions of the WIV Committees Page

This raises the obvious question of why Shi, who served on one of the committees, would lie about military researchers working with the WIV. **Her denial and the scrubbing of the website appear to be obvious attempts to obfuscate the PLA's involvement with the WIV.**

Geospatial Analysis of Traffic Patterns at Wuhan Hospitals Near the WIV

Around the time the WIV's virus database went offline, car traffic at hospitals in downtown Wuhan began to increase. Researchers from Boston University School of Public Health, Boston Children's Hospital, and Harvard Medical School used satellite imagery to examine parking lot volume of hospitals in Wuhan for the two and a half years prior to December 2019. They found that five of six hospitals analyzed had the highest relative daily volume of cars in the parking lot in September and October 2019, before the first reported cases of COVID-19.

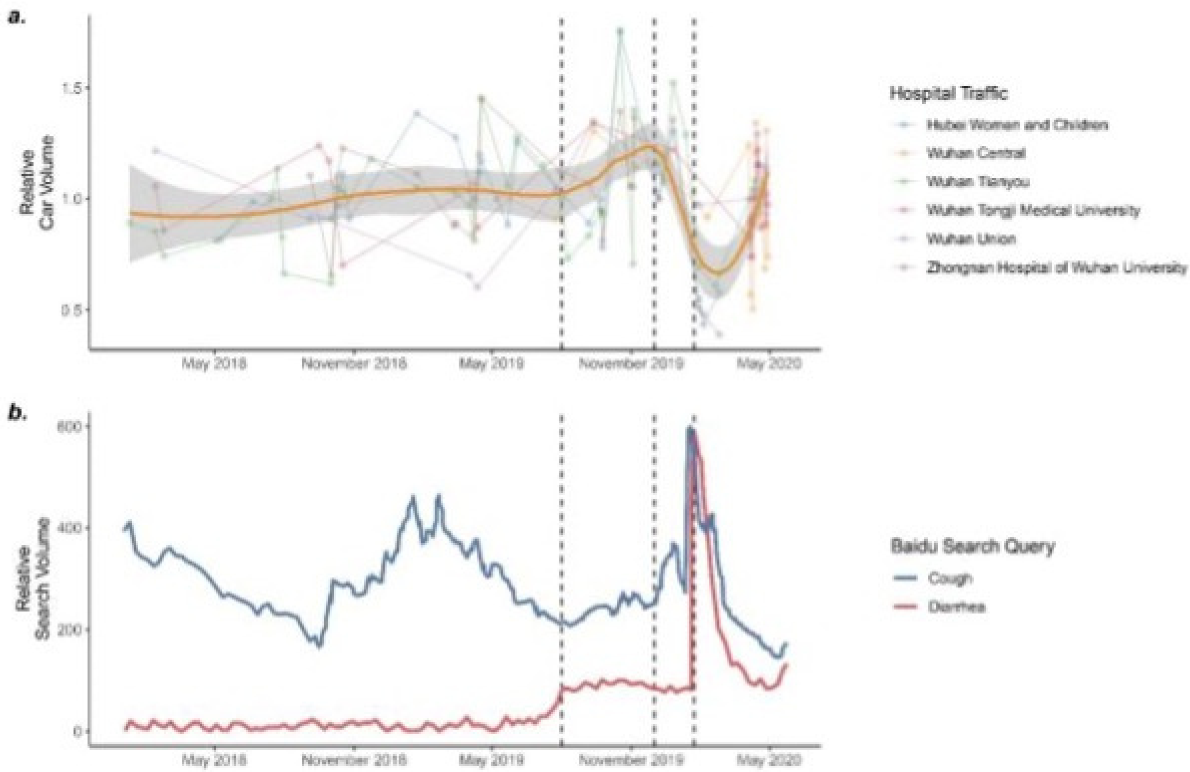


Fig. 7: Time-series of Different Influenza-like Illnesses, Symptoms and Surveillance signals[62]

This peak corresponded with an increase in searches for "cough" and "diarrhea" in Wuhan on Baidu, a Chinese search engine.[60] According to the CDC, both cough and diarrhea are symptoms of COVID-19.[61] This study suggests a virus with similar symptoms as COVID-19 was circulating in Wuhan in September and October.

The Initial Outbreak's Proximity to the WIV

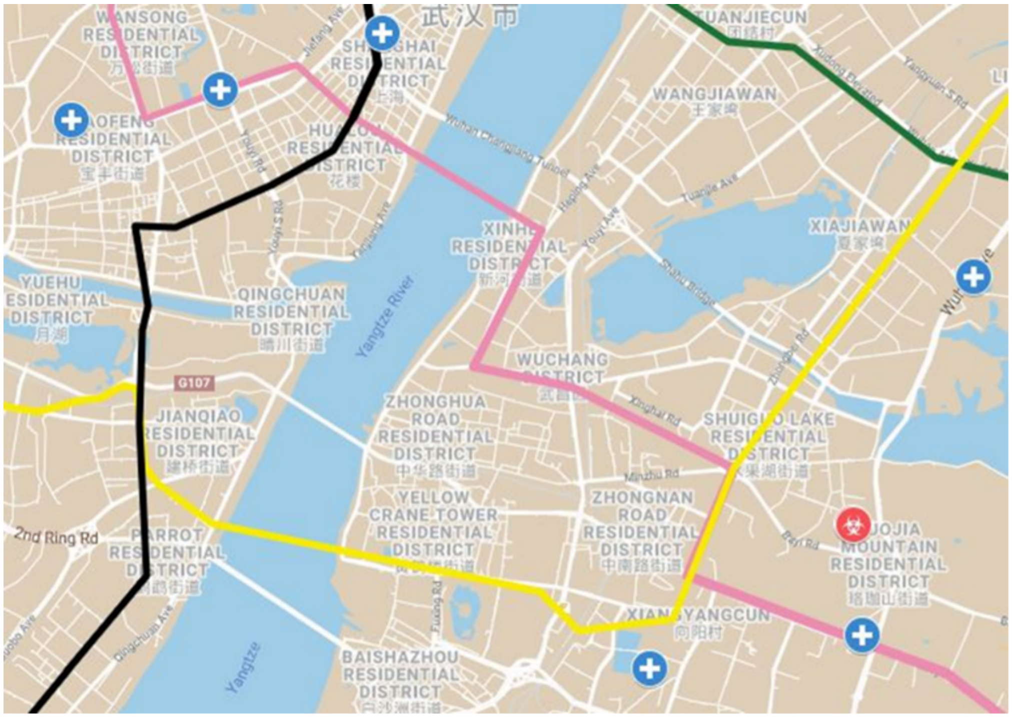
When people get sick, they are likely to seek healthcare near their home or work. Each of the hospitals that saw a rise in traffic with patients complaining of COVID-19 symptoms are located within 6.5 miles of the WIV Headquarters and are connected by public transit lines. The below map shows the location of the WIV Headquarters (in red) and the six hospitals (in blue) which experienced increase vehicle traffic in September and October 2019. When plotted on a map, these six hospitals are clustered around the WIV Headquarters in Wuchang, Wuhan, and are connected to that facility via the Wuhan Metro – various lines are shown in black, yellow, pink, and green on the map. The pink line represents Line 2, whose daily passenger volume exceeded one million trips in 2017.[63]

60 Nsoesie, Elaine Okanyene, et. al. "Analysis of hospital traffic and search engine data in Wuhan China indicates early disease activity in the Fall of 2019 (2020)." *Digital Access to Scholarship at Harvard,* 2020. http://nrs.harvard.edu/urn-3:HUL.InstRepos:42669767

61 "Symptoms of COVID-19." *Centers for Disease Control and Prevention*. https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html

62 Nsoesie

63 "Wuhan Metro is bursting with passengers, breaking records for two consecutive days." 5 April 2017, https://web.archive.org/web/20170825184909/http://ctjb.cnhubei.com/html/ctjb/20170405/ctjb3089625.html



Map 1: Harvard Study Hospitals in Relation to the WIV Headquarters

It is also important to note, according to an Australian scientist who worked in the BSL-4 lab, a daily shuttle bus transfers WIV researchers from the Wuhan Branch of the Chinese Academy of Sciences to the WNBL facility and back again.[64] According to public mapping data, the shuttle pick up and drop off point is less than 500 meters from the WIV Headquarters. As such, it is likely that researchers from both the WIV Headquarters, as well as the WNBL, used the Wuhan metro and/or the WNBL shuttle bus, as part of their daily work commute.

Therefore, it is reasonable to conclude, based on the WIV's extensive sample library and history of genetically manipulating coronaviruses, that in early September, one or more researchers became infected with SARS-CoV-2 in the lab and carried it out into the city. Based on the WIV's publications, researchers could have been exposed while experimenting with a natural virus collected from the wild or infected with a virus they genetically manipulated. Those researchers likely traveled to and from the WIV via the Wuhan metro or via the shuttle service, providing a vector for the virus to spread. This corresponds with the first signs of a growing wave of ill people in Wuhan centered around the WIV's Wuchang facility.

The 2019 Military World Games and Sick Athletes

The 7th International Military Sports Council Military World Games (MWGs) opened in Wuhan on October 18, 2019. The games are similar to the Olympic games but consist of military athletes with some added military disciplines. The MWGs in Wuhan drew 9,308 athletes, representing 109 countries, to compete in 329 events across 27 sports. Twenty-five countries sent delegations of more than 100 athletes, including Russia, Brazil, France, Germany, and Poland.[65]

64 Cortez, Michelle Fay. "The Last—And Only—Foreign Scientist in the Wuhan Lab Speaks Out." *Bloomberg*, 27 June 2021, www.bloomberg.com/news/features/2021-06-27/did-covid-come-from-a-lab-scientist-at-wuhan-institute-speaks-out.

65 "Military Games to Open Friday in China." *China Daily,* 17 Oct. 2019, www.china.org.cn/sports/2019-10/17/content_75311946.htm.

The PRC government recruited 236,000 volunteers for the games, which required 90 hotels, three railroad stations, and more than 2,000 drivers.[66] An archived version of the competition's website from October 20, 2019, lists the more than thirty venues that hosted events for the MWGs across Wuhan and the broader Hubei province.[67] The live website is no longer accessible – it is unclear why it was removed.

During the games, many of the international athletes became sick with what now appear to be symptoms of COVID-19. In one interview, an athlete from Luxembourg described Wuhan as a "ghost town,"[68] and recalls having his temperature taken upon arriving at the city's airport. In an interview with *The Financial Post,* a Canadian newspaper, one member of the Canadian Armed Forces who participated in the games said (emphasis added):

> **This was a city of 15 million people that was in lockdown. It was strange, but we were told this was to make it easy for the Games' participants to get around. [I got] very sick 12 days after we arrived, with fever, chills, vomiting, insomnia.… On our flight to come home, 60 Canadian athletes on the flight were put in isolation [at the back of the plane] for the 12-hour flight. We were sick with symptoms ranging from coughs to diarrhea and in between.**[69]

The service member also revealed his family members became ill as his symptoms increased,[70] a development that is consistent with both human-to-human transmission of a viral infection and COVID-19. Similar claims about COVID-19 like symptoms have been made by athletes from Germany, France, Italy,[71] and Sweden.[72]

By cross referencing the listed MWG venues with publicly available mapping data, it is possible to visualize the venues (in black) in relation to the WIV Headquarters (in red) and the above-mentioned hospitals (in blue). The green figures represent athletes who have publicly expressed their belief they contracted COVID-19 while in Wuhan and are mapped at the venues which hosted the events in which they competed. Some of these athletes resided in the military athletes' village.

> **"[I got] very sick 12 days after we arrived, with fever, chills, vomiting, insomnia.… On our flight to come home, 60 Canadian athletes on the flight were put in isolation [at the back of the plane] for the 12-hour flight. We were sick with symptoms ranging from coughs to diarrhea and in between.**
>
> **- Canadian Athlete"**

66 "2019 Military World Games Kicks off in Central China's Wuhan." *CISION*, 17 Oct. 2019, www.prnewswire.com/news-releases/2019-military-world-games-kicks-off-in-central-chinas-wuhan-300940464.html.

67 "Competition Venues." *Wuhan 2019 Military World Games*, https://web.archive.org/web/20191020154108/en.wuhan2019mwg.cn/html/Competition_venues/.

68 Houston, Michael. "More athletes claim they contracted COVID-19 at Military World Games in Wuhan." *Inside the Games,* 17 May 2020, https://www.insidethegames.biz/articles/1094347/world-military-games-illness-covid-19

69 Francis, Diane. "Diane Francis: Canadian Forces Have Right to Know If They Got COVID at the 2019 Military World Games in Wuhan." *Financial Post,* 25 June 2021, https://financialpost.com/diane-francis/diane-francis-canadian-forces-have-right-to-know-if-they-got-covid-at-the-2019-military-world-games-in-wuhan.

70 *Ibid*.

71 Houston.

72 Liao, George. "Coronavirus May Have Been Spreading since Wuhan Military Games Last October." *Taiwan News*, 13 May 2020, www.taiwannews.com.tw/en/news/3932712.



Map 2: WIV Headquarters, Hospitals, MWG Venues, and Sick Athletes

At least four countries who sent delegations to the MWGs have now confirmed the presence of SARS-CoV-2 or COVID-19 cases within their borders in November and December 2019, before the news of an outbreak first became public.

1. Italy. In February 2021, researchers from Italy published a research letter in the CDC's Emerging Infectious Diseases journal describing a case involving a 4-year-old boy from Milan. A retrospective analysis of samples taken in 2019 identified the boy, who developed a cough on November 21, 2019, as having been infected with SARS-CoV-2 three months before Italy's first reported case. The boy had no reported travel history.[73]

2. Brazil. A March 2021 article by researchers in Brazil examined wastewater samples from October to December 2019. Previous studies have confirmed that humans infected with the virus can experience prolonged viral shedding via their gastrointestinal tract. **A sample from November 27th tested positive for SARS-CoV-2 RNA**, confirming the virus was circulating in Santa Catarina, Brazil months before January 21, 2020, when the first case in the Americas was reported.[74]

3. Sweden. Sweden's Public Health Agency said it is likely that individuals in the country were infected with SARS-CoV-2 as early as November 2019.[75]

73 Amendola, Antonella¸ et. al. "Evidence of SARS-CoV-2 RNA in an Oropharyngeal Swab Specimen, Milan, Italy, Early December 2019." *Emerging Infectious Diseases,* Feb. 2021, 27(2). https://doi.org/10.3201/eid2702.204632

74 Fongaro, Gislaine et al. "The presence of SARS-CoV-2 RNA in human sewage in Santa Catarina, Brazil, November 2019." *The Science of the Total Environment,* 8 March 2021, 778: 146198. https://dx.doi.org/10.1016%2Fj.scitotenv.2021.146198

75 "Coronavirus May Have Arrived in Sweden in November: Public Health Agency." *The Local,* 5 May 2020, www.thelocal.se/20200505/the-coronavirus-may-have-arrived-in-sweden-in-november/.

4. France. Researchers in France also re-tested samples from late 2019 in an effort to identify early COVID-19 cases. They identified a 42-year-old male who presented to the emergency room on December 27th with an influenza-like illness. He had no connection to the PRC and no recent travel history. Upon re-testing, the patient's samples were positive for SARS-CoV-2. It should be noted that one of his children also had similar symptoms before the man became sick, suggesting that the first case in France was likely earlier than December 27th.[76]

As stated above, athletes from France, Italy, and Sweden also complained of illnesses with symptoms similar to COVID-19 while at the MWGs in Wuhan. **The presence of SARS-CoV-2 in four countries, on two separate continents, suggests a common source. If, as presumed, SARS-CoV-2 first infected humans in Wuhan before spreading to the rest of the world, the 2019 Military World Games in Wuhan appears to be a key vector in the global spread – it other words, potentially one of the first "super spreader" events.**

Conclusion

While much of the public debate was initially focused on the Huanan seafood market in Wuhan as the origin of the pandemic, the preponderance of evidence now suggests that the virus leaked from the Wuhan Institute of Virology. Given the WIV's demonstrated history of conducting gain-of-function experiments on coronaviruses, including genetically manipulating viruses specifically to make them infectious to humans in BSL-2 labs, as well as their possession of one of the world's largest collections of coronaviruses, it is completely plausible that one or more researcher(s) was accidentally infected and carried the virus out of the lab. The evidence outlined above, combined the cover-up conducted CCP authorities, strongly suggest the Wuhan Institute of Virology as the source of the current pandemic.

III. EVIDENCE OF GENETIC MODIFICATION

The other topic of debate is whether the virus could have been genetically modified. The WIV was conducting gain-of-function research on coronaviruses and testing them against human immune systems in the months leading up to the emergence of SARS-CoV-2, however the scientific community has claimed it is not possible it was anything but a naturally occurring virus. But, as this report lays out, we believe it is a viable hypothesis that the virus could have been modified.

> **"You can engineer a virus without leaving any trace. The answers you are looking for, however, can only be found in the archives of the Wuhan laboratory."**
>
> **– Dr. Ralph Baric**

76 Deslandes, A et al. "SARS-CoV-2 was already spreading in France in late December 2019." *International Journal of Antimicrobial Agents,* 3 May 2020, 55(6): 106006. https://dx.doi.org/10.1016%2Fj.ijantimicag.2020.106006

77 Stahl, Lesley. "What Happened In WUHAN? Why Questions Still Linger on the Origin of the Coronavirus." *CBS News*, 28 Mar. 2021, www.cbsnews.com/news/covid-19-wuhan-origins-60-minutes-2021-03-28/.

Research Regarding SARS Like Coronaviruses from 2004-2017



The WIV's work on bat coronaviruses dates back to the aftermath of SARS in the early 2000s. Shi met Peter Daszak, an American citizen, in 2004 during an effort to find the origins of the 2002 SARS pandemic. Daszak is the CEO of EcoHealth Alliance, a New York-based NGO that funds scientific research around the world.[78] For the last year and a half, questions have been raised about how and why EcoHealth Alliance provided the WIV with U.S. taxpayer dollars. Those funds were provided to EcoHealth Alliance in the form of grants from the Department of Health and Human Services (HHS), National Institutes of Health (NIH), National Science Foundation (NSF), and the United States Agency for International Development (USAID).

Beginning in 2005, and continuing over the next 16 years, Shi and Daszak have collaborated on coronavirus research. Together, they "led dozens of expeditions to caves full of bats, to collect samples and analyze them."[79] They have identified more than 500 novel coronaviruses, including roughly 50 related to SARS or MERS, and they have repeatedly engaged in gain-of-function research on coronaviruses designed to make them more infectious in humans.[80] As discussed below, the vast majority of the most relevant scientific publications that have emerged from the WIV regarding coronaviruses was conducted with funding provided by Peter Daszak through EcoHealth Alliance.

Article and Publication: "Bats Are Natural Reservoirs of SARS-Like Coronaviruses," in Science (2005).

Participants: Li Wendog, primary author; Shi, second author and one of three corresponding authors; Peter Daszag; additional scientists from Australia and China.

Funding: The paper was supported in part by funding from the PRC government, who provided a special grant for Animal Reservoirs of SARS-CoV from the State Key Program for Basic Research (grant no. 2005CB523004) and the State High Technology Development Program (grant no. 2005AA219070) from the Ministry of Science and Technology.

78 Zaugg, Julie. "In Wuhan with Bat Woman, at the origins of the Covid-19." *L'Illustre*, 22 Jan. 2021, https://www.illustre.ch/magazine/a-wuhan-avec-bat-woman-aux-origines-du-covid-19

79 *Ibid.*

80 *Ibid.*

It was also funded by the U.S. government, through the NIH and NSF, who provided funding in the form of an 'Ecology of Infectious Diseases'' award (no. R01-TW05869) from the John E. Fogarty International Center and the V. Kann Rasmussen Foundation.

Purpose: The scientists hoped to identify the origins of SARS by identifying species of bats which are a natural host for SARS-like coronaviruses.

Conclusion: "These findings on coronaviruses, together with data on henipaviruses (23–25, 28), suggest that genetic diversity exists among zoonotic viruses in bats, increasing the possibility of variants crossing the species barrier and causing outbreaks of disease in human populations. It is therefore essential that we enhance our knowledge and understanding of reservoir host distribution, animal-animal and human-animal interaction (particularly within the wet-market system), and the genetic diversity of bat-borne viruses to prevent future outbreaks."[81]

Relevance: This conclusion would drive the next fifteen years of collaboration between the WIV and Peter Daszak, with Shi directing the laboratory work.

In 2006, Shi and Daszak collaborated with a researcher in Australia to publish "Review of bats and SARS" in Emerging Infectious Diseases, a peer-reviewed journal published monthly by the U.S. Centers for Disease Control and Prevention. Shi was again listed as the second author, and the work was funded by the same PRC and NIH/NSF grants referenced above.[82] The following year, these grants supported the publication of "Evolutionary Relationships between Bat Coronaviruses and Their Hosts" in Emerging Infectious Diseases. Shi is listed as the sixth author, followed by another WIV researcher, and Peter Daszak is listed as one of two corresponding authors.[83]

In 2007, Shi and several other WIV researchers joined additional scientists in publishing another paper on coronaviruses.

Article and Publication: "Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin" in Journal of Virology.

Participants: WIV researchers and Linfa Wang. Shi is listed as the corresponding author.

Funding: This work was funded by the PRC government and grants from Australia and the European Commission.

Purpose: This study focused on the receptors used by the spike protein of SARS-like coronaviruses, which are the major surface structures that enable coronaviruses to bind to receptors on cells. To test this, researchers created multiple chimeric viruses by inserting different sequences of the SARS-CoV spike protein into the spike protein of the SARS-like virus being examined, and tested them against bat, civet, and human ACE2 expressing cells.

Conclusion: One of these chimeric viruses was able to enter cells through the human ACE2 receptor. ACE2 is an abbreviation for angiotensin converting enzyme-2, which is a protein found on the surface of cells and tissues throughout the human body,

81 *Ibid.*

82 Wang L-F, Shi Z, Zhang S, Field H, Daszak P, Eaton BT. "Review of bats and SARS." *Emerg Infect Dis,* Dec. 2006; 12(12): 1834-1840., http://dx.doi.org/10.3201/eid1212.060401

83 Cui J, et. al. "Evolutionary relationships between bat coronaviruses and their hosts." *Emerg Infect Dis*., Oct. 2007; 13(10):1526-32. https://wwwnc.cdc.gov/eid/article/13/10/07-0448_article

including the nose, mouth, and lungs. "In the lungs, ACE2 is highly abundant on type 2 pneumocytes, an important cell type present in chambers within the lung called alveoli, where oxygen is absorbed and waste carbon dioxide is released."[84] ACE2 is also the location where SARS-CoV-2's spike protein binds to human cells. Researchers concluded that "a minimal insert region" is "sufficient to convert the SL-COV S [SARS-like coronavirus spike protein] from non-ACE2 binding to human ACE2 binding." [85]

Relevance: In other words, WIV researchers were able to take a SARS-like coronavirus that does not infect humans and modify it so it was able to do so. Also importantly, this work was done under BSL-2 conditions.

Shi and Daszak do not appear as coauthors on a paper again until 2013.

Article and Publication: "Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor" in *Nature*.[86]

Participants: WIV and EcoHealth researchers, including Hu,. Shi, Daszak, and Wang who are credited for designing the experiments. Shi and Daszak listed as corresponding authors.

Funding: The study was funded by grants from the PRC government (including grant no. 2013FY113500), as well as the National Institute of Allergy and Infectious Diseases (NIAID) (no. R01AI079231), a NIH/NSF "Ecology and Evolution of Infectious Diseases" award (no. R01TW005869), an award from the NIH Fogarty International Center supported by International Influenza Funds from the Office of the Secretary of the Department of Health and Human Services (no. R56TW009502), and USAID's Emerging Pandemic Threats PREDICT program.[87]

Purpose: This work marked "the first recorded isolation of a live SL-CoV"[88] [SARS-live coronavirus], which researchers isolated from bat fecal samples and named WIV1. Additionally, they identified two novel bat coronaviruses (SCH014 and Rs3367) and reported "the first identification of a wild-type bat SL-CoV capable of using ACE2 as an entry receptor."[89]

Conclusion: "Finally, this study demonstrates the public health importance of pathogen discovery programs targeting wildlife that aim to identify the 'known unknowns'—previously unknown viral strains closely related to known pathogens. These programs, focused on specific high-risk wildlife groups and hotspots of disease emergence, may be a critical part of future global strategies to predict, prepare for, and prevent pandemic emergence." [90]

Relevance: By isolating a wild-type (common strain in nature) SARS-like coronavirus that binds to ACE2, and testing it in human lung tissue, the authors proved that bat coronaviruses are capable of infecting humans directly, without having to pass through an intermediate host.

84 *S*riram, Krishna, et al. "What Is the ACE2 Receptor, How Is It Connected to Coronavirus and Why Might It Be Key to Treating COVID-19? The Experts Explain." The Conversation, 25 May 2021, https://theconversation.com/what-is-the-ace2-receptor-how-is-it-connected-to-coronavirus-and-why-might-it-be-key-to-treating-covid-19-the-experts-explain-136928.

85 Ren.

86 Ge, Xing-Yi et al. "Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor." *Nature,* 30 Oct. 2013, 503(7477): 535-8. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5389864/

87 *Ibid.*

88 *Ibid.*

89 *Ibid.*

90 *Ibid.*

In 2014, Shi and Daszak coauthored two more joint WIV-EcoHealth Alliance papers. The lead author for one of the papers, entitled "Detection of diverse novel astroviruses from small mammals in China," was Ben Hu, a WIV researcher who was a coauthor of earlier Shi/Daszak papers. Shi is listed as the corresponding author, and the paper was again jointly funded by the PRC government (including grant no. 2013FY113500) and USAID's PREDICT program.[91]

The next year, in 2015, Shi provided Ralph Baric and other researchers at the University of North Carolina at Chapel Hill with spike protein sequences and plasmids of SCH014, one of the viruses Shi, Daszak, and WIV researchers identified in bat feces samples in 2013. American researchers used those samples to create "a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone."[92] **In other words, they removed the spike protein from SHC014 and inserted it into a SARS coronavirus that was genetically manipulated to better infect mice.** This work was done under BSL-3 conditions. The newly created virus was then shown to bind to ACE2 in humans, replicate "efficiently"[93] in primary human airways cells, and withstand antibodies and vaccines. Researchers concluded that the work "suggests a potential risk of SARS-CoV re-emergence from viruses currently circulating in bat populations."[94] This research was funded by NIAID and the NIH under multiple awards (nos. U19AI109761, U19AI107810, AI085524, F32AI102561, K99AG049092, DK065988), USAID's PREDICT program via EcoHealth Alliance, and the PRC government. Baric was the corresponding author.[95]

2015 also saw the publication of another Shi/Hu/Wang/Daszak paper. Entitled "Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus," it was published in the *Journal of Virology.* Nine of the twelve authors were WIV researchers, including Hu and Shi, who was the corresponding author. Here the WIV reported the successful isolation of a second novel coronavirus, WIV16. The SARS-like coronavirus was isolated from a single sample of bat fecal matter collected in Kunming, Yunnan Province of the PRC in July 2013. Like previous papers, this work was supported by a NIAID grant (no. R01AI110964) and by grants from the PRC government (including grant no. 2013FY113500).[96]

In addition to her aforementioned work with researchers at UNC Chapel Hill, Shi also provided them with additional bat coronavirus sequences and plasmid of WIV1's spike protein. The resulting paper, "SARS-like WIV1-CoV poised for human emergence," was published in the Proceedings of the National Academy of Sciences of the United States of America in March 2016. While neither Shi nor Daszak (nor any WIV researcher) are listed as coauthors, Baric was the corresponding author.

91 Hu, Ben, et. al. "Detection of diverse novel astroviruses from small mammals in China." *J Gen Virol.* Nov 2014, 95(Pt 11): 2442-2449. https://pubmed.ncbi.nlm.nih.gov/25034867/

92 Menachery, Vineet, et. al. "A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence." *Nat Med,* 9 Nov. 2015, 21:1508–1513. https://doi.org/10.1038/nm.3985

93 Menachery

94 *Ibid.*

95 *Ibid.*

96 Yang, Xing-Lou et al. "Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus." *Journal of Virology,* 30 Dec. 2015, 90(6): 3253-6. https://dx.doi.org/10.1128%2FJVI.02582-15

This paper is significant because the authors discuss moving from disease surveillance to creating chimeric viruses as a means of pandemic preparedness; "this manuscript describes efforts to extend surveillance beyond sequence analysis, constructing chimeric and full-length zoonotic coronaviruses to evaluate emergence potential." [97]

During this work, researchers produced chimeric viruses created by inserting the spike protein from WIV1 into a strain of SARS-CoV adapted to infecting mice. They subsequently tested this chimeric virus in human airway epithelial cells as well as in mice.[98] In addition to standard BALB/c mice (a strain of albino, lab-breed house mice used in experimentation[99]), researchers genetically manipulated the mice to create a strain of mice expressing the human ACE2 (hACE2) receptor. While hACE2 was found primarily in the lungs of the mice, it was also present in the brain, liver, kidneys, and gastrointestinal tract. The WIV1 chimeric virus was then tested in these hACE2 expressing mice, proving that the chimeric virus could infect humans. This work was funded by NIAID and NIH awards (nos. U19AI109761, U19AI107810, AI1085524, F32AI102561, K99AG049092, DK065988, AI076159, and AI079521).[100]

In 2016, Shi and Daszak also coauthored two additional papers focused on infectious diseases that year. One, entitled "Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response," was coauthored by Wang and represents a major step forward in the WIV's work. While working on this project, WIV researchers created a reverse genetics system and used it to genetically modify WIV1, the live coronavirus that was successfully isolated in 2013 and that UNC researchers manipulated months earlier. WIV researchers created multiple versions of this virus by deleting or adding genetic information to the virus' RNA. According to the paper, all experiments with live virus for this paper were done under BSL-2 conditions, which does not require respirators or biological safety cabinets. Nine of the eleven authors are WIV researchers, and Shi is the corresponding author. The experimentation for the paper was supported by a grant from NIAID (no. R01AI110964) and funding from the PRC government.[101]

The following year, Ben Hu was the lead author of a paper entitled "Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus." As with previous papers, the overwhelming majority (14 out of 17) of the authors worked at the WIV. Daszak, Shi, and Wang are all listed as coauthors. Hu is the lead author and Shi is one of two corresponding authors. Daszak is credited for "funding acquisition."[102]

Additionally, using the reverse genetics system they debuted the previous year, WIV researchers created eight separate chimeric viruses by inserting the spike protein of various SARS-like coronaviruses into WIV1. Two of these chimeric viruses (WIV1-Rs4231S and WIV1-Rs7327S), and one natural virus, Rs4874, all replicated within hACE2 expressing cells.[103]

97 Menachery, Vineet, et al. "SARS-like WIV1-CoV poised for human emergence." *Proceedings of the National Academy of Sciences of the United States of America,* 14 March 2016, 113(11): 3048-53. https://dx.doi.org/10.1073%2Fpnas.1517719113

98 *Ibid.*

99 "Inbred Strains: BALB." MGI, www.informatics.jax.org/inbred_strains/mouse/docs/BALB.shtml.

100 Menachery 2016.

101 Zeng, Lei-Ping et al. "Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response." *Journal of Virology,* 24 June 2016, 90(14): 6573-6582. https://dx.doi.org/10.1128%2FJVI.03079-15

102 Hu, Ben et al. "Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus." *PLOS Pathogens,* 30 Nov. 2017, 13(11). https://dx.doi.org/10.1371%2Fjournal.ppat.1006698

103 Hu, 2017.

To reiterate, WIV researchers created chimeric coronaviruses able to infect humans in 2017, before the WNBL BSL-4 lab became operational. This work was jointly funded by NIAID (no. R01AI110964), USAID's PREDICT program, and the PRC government (including grant no. 2013FY113500).

Research Regarding SARS-Like Coronaviruses at the WIV or in Conjunction with WIV Scientists from 2018-2019

While Shi and Daszak coauthored several additional papers in 2018 and 2019 regarding coronaviruses, none include gain-of-function research on SARS-like coronaviruses designed to make them more infectious to humans. This is especially odd given that in 2018 the Chinese Academy of Science launched a new special project titled "Pathogen Host Adaption and Immune Intervention."[104] One of the five subprojects was titled "Research on Virus Traceability, Cross-Species Transmission, and Pathogenic Mechanism," – Shi is listed as one of the two scientists in charge.[105] This subproject had three areas of focus: 1) the traceability, evolution and transmission mechanism of new pathogens; 2) molecular mechanisms of viral cross-species infection and pathogenicity, and 3) the interaction mechanism between virus and host.

A second WIV scientist, Cui Zongqiang, was one of two researchers in charge of another subproject entitled, "New methods and new technologies for infection and immune research."[106] This project focused on, among other things, evaluating new vaccines and establishing "humanized small animal models"[107] for in vitro pathogen testing.[108]

In January 2018, Shi was appointed Principal Investigator for a new Strategic Priority Research Program of the Chinese Academy of Sciences (grant no. XBD29010101, $1.35 million USD), investigating "genetic evolution and transmission mechanism of important bat-borne viruses."[109] This project, especially with its focus on transmission mechanisms, aligns with the first focus area mentioned above. That same month, Shi began work on a project titled "Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of cross-species infection."[110] The project was funded at a value of roughly $850,000 USD (grant no. 31770175) and is slated to run until December 2021.[111] This grant aligns with the second focus area, the description of which specifically mentions replicating and modifying coronaviruses (emphasis added):

> For important emerging emergencies and virulent viruses (influenza virus, Ebola virus, coronavirus, Marburg virus, arenavirus, etc.), by studying **their ability to invade different host cells and their ability to replicate in different host cells,** analyze the key molecules affecting their cross-species infections and their pathogenic mechanisms. Including: virus invasion, virus replication and assembly, and infection model.[112]

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104 "Guidelines for the application of the 'Pathogen Host Adaptation and Immune Intervention' project of the Chinese Academy of Sciences Strategic Leading Technology." Chinese Academy of Sciences, 6 Sept. 2018, https://archive.is/spmNg#selection-3389.0-3389.160

105 *Ibid.*

106 *Ibid.*

107 *Ibid.*

108 *Ibid.*

109 Shi, Zheng-li. "Curriculum Vitae." https://www.ws-virology.org/wp-content/uploads/2017/11/Zhengli-Shi.pdf

110 "Study on the evolutionary mechanism of bat SARS-like coronavirus adapted to host receptor molecules and the risk of cross-species infection." *MedSci*, https://archive.is/g35C6#selection-1425.0-1425.139

111 *Ibid.*

112 "Guidelines for the application of the 'Pathogen Host Adaptation and Immune Intervention' project of the Chinese Academy of Sciences Strategic Leading Technology." *Chinese Academy of Sciences,* 6 Sept. 2018, https://archive.is/spmNg#selection-3389.0-3389.160

Shi did not publish any papers funded by this grant before the start of the pandemic. As such, it is impossible to know what experiments she was conducting in the months prior to the pandemic.

Further evidence expands on Shi's work in 2018 and 2019. In January 2019, Shi and several other scientists were awarded a National Natural Science Award Second Prize for a project entitled, "Research on Important Viruses Carried by Chinese Bats."[113] Five out of the six researchers on the award were coauthors of the previously discussed 2013 paper entitled, "Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor."

In January 2019, Ben Hu, was awarded $385,850 in grant money (grant no. 31800142) by the Youth Science Fund Project (YSFP) of the National Natural Science Foundation of China.[114] The YSFP "supports the young researchers to independently select topics within the scope of the scientific funding and carry out basic research."[115] This project, selected by Ben Hu, was titled, "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2."[116] To date, the two novel SARS-related coronaviruses have not been identified, and the grant money has only been cited in papers published about SARS-CoV-2.

WIV researchers confirmed to the WHO investigative team that they were conducting experimentations testing chimeric coronaviruses in 2018 and 2019.[117] According to an interview with Shi published by *Science*, all coronavirus experimentation, including infecting hACE2 mice and civets, was done at the BSL-2 and BSL-3 levels – "the coronavirus research in our laboratory is conducted in BSL-2 or BSL-3 laboratories." [118]

This ongoing work appears to coincide with Peter Daszak's stated goal of developing a broad-spectrum coronavirus vaccine. In a May 19, 2020, interview with "This Week in Virology," Daszak discussed the goal of the gain-of-function work he funded on coronaviruses with the WIV (emphasis added):

> Coronaviruses are pretty good – I mean you're a virologist, you know all this stuff – but the… you can... um manipulate them in the lab pretty easily. The spike protein drives a lot of what happens with the coronavirus – zoonotic risk. So, you can get the sequence, you can build the protein, and we work with Ralph Baric at UNC to do this, insert it into a backbone of another virus, and do some work in the lab. So, you can get more predictive when you find a sequence – you've got this diversity. Now, the logical progression for vaccines is, if you're going to develop a vaccine for SARS, people are going to use pandemic SARS, **but let's try to insert some of these other related [viruses] and get a better vaccine.**

113 "Catalogue and introduction of the 2018 National Natural Science Award winning projects." *Ministry of Science and Technology,* 8 Jan. 2019, https://archive.is/jKq7B#selection-187.0-187.86

114 "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2." *MedSci*, https://archive.is/shrM2#selection-1545.0-1558.0

115 "[Good News] 100% winning bid! All applications of the National Natural Science Foundation of China(NSFC) were approved." F*aculty of Economics and Management, ECNU Academy of Statistics and Interdisciplinary Sciences*, 11 May 2020, http://asis.ecnu.edu.cn/asisenglish/64/ba/c23635a287930/page.htm

116 "Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2." *MedSci*, https://archive.is/shrM2#selection-1545.0-1558.0

117 Joint Report – ANNEXES.

118 Shi, Zheng-li. "Reply to Science Magazine." *Science Magazine*, https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf

119 Racaniello, Vincent. "TWiV 615: Peter Daszak of EcoHealth Alliance." YouTube, interview by Vincent Racaniello,19 May 2020, https://www.youtube.com/watch?v=IdYDL_RK--w

Shi, Hu, and others at the WIV were the ones collecting, identifying, genetically modifying, and testing these novel coronaviruses against human immune systems for Peter Daszak.

In sum, in the years leading up to the emergence of SARS-CoV-2, there was:

- **Research by Shi and others at the WIV on how to alter the spike protein of non-infectious SARS-like coronaviruses so that they can bind to human ACE2 receptors;**
- **Repeated collaboration between Shi, Hu, Daszak, Wang, and other researchers on genetically manipulating coronaviruses to increase their infectiousness in humans;**
- **A new PRC Strategic Priority Research Program, run by Shi, that was actively manufacturing chimeric viruses in BSL-2 and BSL-3 conditions and seeking out novel viruses;**
- **Evidence of ongoing collaboration between Shi and the other scientists who first isolated a live coronavirus in 2013;**
- **A second grant awarded to Hu to test novel coronaviruses against human immune systems in BSL-2 and BSL-3 conditions;**
- **A stated effort to develop a broad-spectrum coronavirus vaccine.**

Given the above, it is self-evident that Shi and her colleagues, with funding and support from Daszak, were actively genetically manipulating coronaviruses and testing them against human immune systems in 2018 and 2019, before the beginning of the pandemic.

Unusual Features of SARS-CoV-2

Committee Minority Staff interviews with scientists and current and former U.S. government officials raised several questions about the natural origins of SARS-CoV-2, including:

1. The highly infectious nature of SARS-CoV-2, which they consider as infectious as measles;
2. The lack of an identified intermediate host (found 4 months after the outbreak of SARS and 9 months after MERS); and
3. The highly efficient binding to human ACE2.

The highly contagious nature of SARS-CoV-2 has been a hot topic of conversation since the virus began to spread around the world. Some scientists and other experts point to the incredibly high case numbers as evidence that SARS-CoV-2 is inherently different from known natural betacoronaviruses. For example, MERS first appeared in 2012 and has infected less than 4,000 people. SARS first appeared in 2002 and infected less than 10,000. At the time of writing, less than two years from when it has first appeared, SARS-CoV-2 has infected more than 196.4 million people.

SARS-CoV-2 also has a highly unusual affinity for binding to human ACE2 receptors over other hosts. In February 2020, American researchers examined this issue closely. They found that SARS-CoV-2's spike protein "binds at least 10 times more tightly than the corresponding spike protein of severe acute respiratory syndrome (SARS)–CoV to their common host cell receptor."[120] In other words, SARS-CoV-2 binds more than 10 times more tightly to human ACE2 than the virus that causes SARS. The researchers found this likely explains why the virus is so contagious.[121]

120 Wrapp, Daniel et al. "Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation." *Science,* 13 March 2020, 367(6483): 1260-1263. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7164637/

121 *Ibid.*

Australian and British researchers also examined how SARS-CoV-2 binds to the ACE2 of various animals, publishing their research in *Scientific Reports* on June 24, 2021. The scientists found that SARS-CoV-2's spike protein binds the strongest to human ACE2. They reported (emphasis added):

> This finding was surprising as a **zoonotic virus typically exhibits the highest affinity initially for its original host species,** with lower initial affinity to receptors of new host species until it adapts. As the virus adapts to its new host, mutations are acquired that increase the binding affinity for the new host receptor. Since **our binding calculations were based on SARS-CoV-2 samples isolated in China from December 2019,** at the very onset of the outbreak, the extremely high affinity of S protein for human ACE2 was unexpected.[122]

The first preprint version of this paper went further, concluding, "the data indicates that SARS-CoV-2 is uniquely adapted to infect humans, **raising important questions as to whether it arose in nature by a rare chance event or whether its origins might lie elsewhere"** emphasis added.[123] **This research provides evidence that SARS-CoV-2 is uniquely well adapted to humans, suggesting a non-zoonotic source of the outbreak.**

The Furin Cleavage Site

One of the most discussed questions centers around the furin cleavage site (FCS) of SARS-CoV-2. The FCS is part of the virus' spike protein, which enables it to bind to and enter human cells. In February 2020, French and Canadian scientists reported SARS-CoV-2 contains an FCS that is absent in other coronaviruses of the same clade, or branch of viruses believed to have a similar common ancestor. The scientists also reported that when a bronchitis virus was modified by inserting a similar cleavage site, the virus' pathogenicity was increased.[124] While some scientists have noted that other coronaviruses contain furin cleavage sites, phylogenetic analysis shows that SARS-CoV-2 is the only identified sarbecovirus (a subsection of *betacoronaviruses*) with this feature.[125]

In January 2021 a group of American researchers published "Loss of furin cleavage site attenuates SARS-CoV-2 pathogenesis" in *Nature*. In the article, researchers reported the FCS "may have facilitated the emergence of SARS-CoV-2 in humans."[126] Using a reverse genetic system, they created a mutant strain of SARS-CoV-2 which lacked the FCS. The result was a virus that was weakened in human respiratory cells and that exhibited reduced development in hACE2 expressing mice. This demonstrates the importance of the FCS in the rapid spread of COVID-19.

122 Piplani, S., et. al. "In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin." *Scientific Reports,* 24 June 2021, 11(13063) https://www.nature.com/articles/s41598-021-92388-5

123 Piplani, S., et. al. Preprint of "In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin." *ArXiv*, 13 May 2020, https://arxiv.org/abs/2005.06199v1

124 Coutard, B et al. "The spike glycoprotein of the new coronavirus 2019-nCoV contains a furin-like cleavage site absent in CoV of the same clade." *Antiviral Research,* Feb. 2020, 176: 104742 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7114094/

125 Wu, Yiran, and Suwen Zhao. "Furin cleavage sites naturally occur in coronaviruses." *Stem Cell Research,* 9 Dec. 2020, 50:102115. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7836551/

126 Johnson, B.A., et. al. "Loss of furin cleavage site attenuates SARS-CoV-2 pathogenesis." *Nature*, 25 Jan. 2021, 591: 293-299. https://www.nature.com/articles/s41586-021-03237-4

In other words, did the FCS develop naturally, or was it added in via genetic manipulation? Part of the genetic sequence for the FCS includes a CGG double codon (CGG-CGG). This group of six nucleotides (a group of three nucleotides is also known as a codon) is half of the 12 nucleotides that create the FCS. SARS-CoV-2 is the only identified coronavirus within its class to feature this combination. Some believe this is evidence of genetic manipulation, arguing this double codon is a telltale sign of the FCS being artificially inserted into the virus.[127]

The "No-See-Um" Method

Critics of the theory that the virus was genetically modified or man-made have repeatedly pointed to the apparent lack of telltale signs of genetic manipulation in the SARS-CoV-2 genome. They claim this is "proof" the virus was not only naturally occurring, but that the COVID-19 pandemic could only be the result of a zoonotic spillover event. Such arguments ignore key pieces of evidence to the contrary.

In 2005, Ralph Baric, one of the researchers at UNC Chapel Hill with whom Shi would later collaborate with between 2014 and 2016, published a paper entitled, "Development of mouse hepatitis virus and SARS-CoV infectious cDNA constructs."[128] In this paper, Baric references using a novel genetic engineering system he developed with other UNC colleagues to engineer full-length SARS-CoV genomes via a "no-see-um" method. This method allows for the assembly of various partial genomic sequences into a full-length genome, creating a new and infectious coronavirus.[129] The publication includes the below figure, which is titled, "Systemic Assembly Strategy for the SARS-CoV infectious clone." It clearly shows the various SARS fragments and how they were used to create a full-length, custom genomic sequence.

> **Molecularly cloned viruses were indistinguishable from wild type.**
>
> **– Dr. Ralph Baric**

127 Quay, Steven, and Richard Muller. "The Science Suggests a Wuhan Lab Leak." *The Wall Street Journal*, 6 June 2021, www.wsj.com/articles/the-science-suggests-a-wuhan-lab-leak-11622995184.

128 Baric R.S., Sims A.C. "Development of Mouse Hepatitis Virus and SARS-CoV Infectious cDNA Constructs." *Curr Top Microbiol Immunol,* 2005; 287:229-52. https://doi.org/10.1007/3-540-26765-4_8

129 *Ibid.*

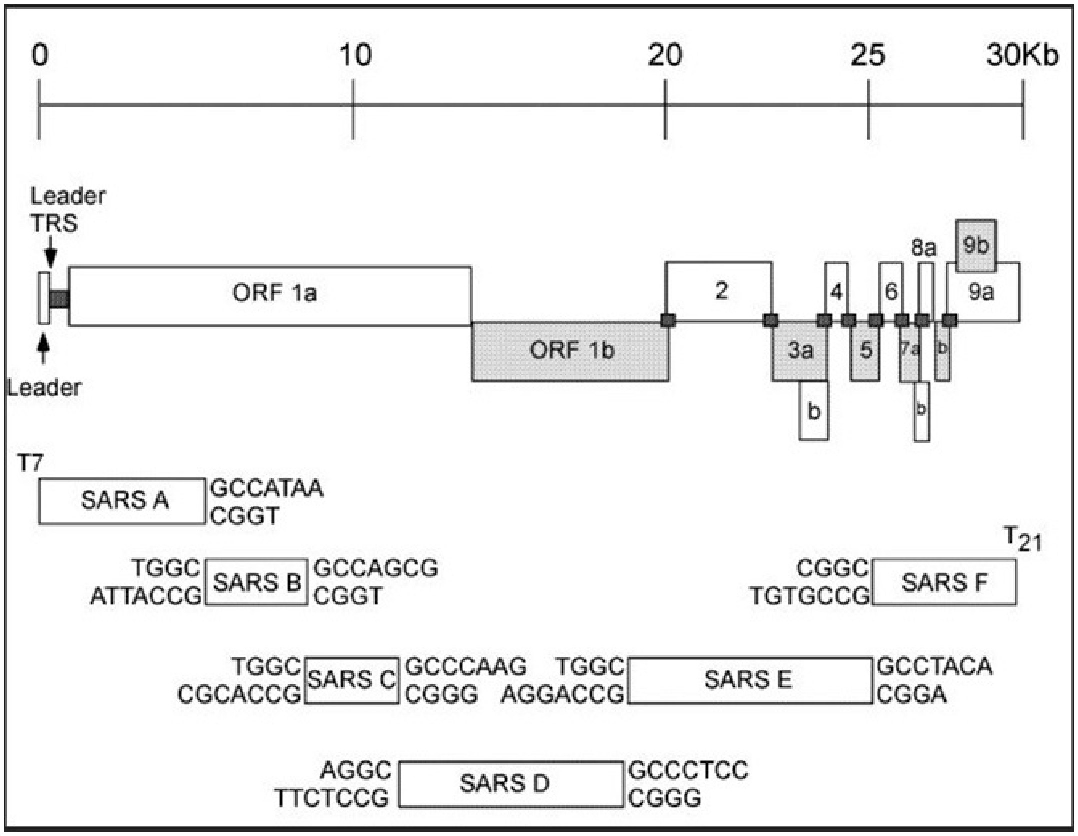


Fig. 5: Baric's "No-See-Um" System

The paper stated these viruses were "indistinguishable from wild type," [130] meaning that it is impossible to tell they were synthetically created.

Baric himself confirmed this interpretation in a September 2020 interview, where he stated, "You can engineer a virus without leaving any trace. The answers you are looking for, however, can only be found in the archives of the Wuhan laboratory." [131] Referring to chimeric viruses he generated in 2015 with WIV researchers, Baric said his team intentionally left signature mutations to show that it was genetically engineered. "Otherwise there is no way to distinguish a natural virus from one made in the laboratory." [132]

Shi and Baric have collaborated on multiple papers regarding coronaviruses. The most recent of which was in May 2020, when they joined other researchers in publishing "Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2." [133] **One year later, Baric signed onto a May 14, 2021, letter published in *Science* which argued that the lab leak theory must be taken seriously and should be fully evaluated.**[134]

130 *Ibid.*

131 Renda, Silvia. "Possibile Creare Un Virus in Laboratorio Senza Lasciare Traccia? La Risposta Dell'autore Della Chimera Del 2015 Di Cui Parlò Tg Leonardo." *L'HuffPost,* 14 Sept. 2020, www.huffingtonpost.it/entry/e-possibile-creare-un-virus-in-laboratorio-senza-lasciare-traccia-la-risposta-dellesperto_it_5f5f3993c5b62874bc1f7339.

132 *Ibid.*

133 Jiang, Ren-Di et al. "Pathogenesis of SARS-CoV-2 in Transgenic Mice Expressing Human Angiotensin-Converting Enzyme 2." *Cell*, 21 May 202, 182(1): 50-58.e8, https://dx.doi.org/10.1016%2Fj.cell.2020.05.027

134 Bloom, Jesse D., et. al. "Investigate the origins of COVID-19." *Science*, 14 May 2021; 372(6543): 694. https://science.sciencemag.org/content/372/6543/694.1

In 2017, a dissertation was submitted to the University of Chinese Academy of Sciences by Zeng Leiping, a doctoral student working at the WIV, entitled "Reverse Genetic System of Bat SARS-like Coronaviruses and Function of ORFX."[135] The referenced reverse genetic system is the same that was used by the WIV in 2016 to create genetically modified viruses and conduct experiments with live viruses under BSL-2 conditions. In his dissertation, Zeng stated the he and other WIV researchers used this system to "construct an S gene chimeric recombinant viral infectious BAC clone with WIV1 as the backbone and without leaving any trace sequences (e.g. incorporated enzymatic sites) in the recombinant viral genome" (emphasis added).

In an end-of-chapter discussion in the dissertation, Zeng reiterates this lack of evidence of genetic manipulation, stating:

> We established a reverse genetics system for coronaviruses, and based on the genomic backbone of WIV1, we **established a scheme to replace the S gene without traces,** constructed infectious BAC clones of 12 S-gene chimeric recombinant viruses, and successfully rescued. Four of these recombinant viral strains (including Rs4231, Rs4874, Rs7327, and SHC014) were tested for ACE2 utilization by these strains in humans, civets, and bats.

Zeng was employed at the WIV when he submitted his dissertation, and Shi was his advisor. **As such, it is clear that Shi and others at the WIV not only possessed the capability to genetically modify coronaviruses "without traces," but were actively doing so in the years leading up to the current pandemic.** It appears Zeng Leiping is currently a postdoctoral research fellow in bioengineering at Stanford University.

IV. EVIDENCE OF A LAB LEAK COVER-UP

In addition to the events previously discussed (sequence database taken offline, road closures during the MWG, etc.), there are several additional incidents that suggest the PRC, WIV researchers, and others were actively working to suppress and discredit early conversations that the virus could have been man-made or that it could have leaked from a WIV facility.

In April 2012, six miners working in a copper mine located in Yunnan province of the PRC fell ill. Between the ages of 30 and 63, the workers presented to a hospital in Kunming with "persistent coughs, fevers, head and chest pains and breathing difficulties."[139] Three of the six eventually died. Researchers from the WIV were asked to investigate and test samples from the sick miners. They also began collecting samples from bats in the cave that housed the mine, which led to the discovery of several new coronaviruses. As a result, the WIV began a long-term study of the mine, collecting samples each year. Despite this, Shi maintains the miners were killed by a fungus growing on bat feces not from a virus.[140]

135 Leiping, Zeng. *Reverse Genetic System of Bat SARS-like Coronaviruses and Function of ORFX.* 2017. The University of Chinese Academy of Sciences, PhD dissertation. English translation first made available by @TheSeeker268 on Twitter, https://twitter.com/TheSeeker268/status/1392575597772107776?s=20

136 *Ibid.*

137 *Ibid.*

138 "Leiping Zeng." *Stanford*, https://profiles.stanford.edu/leiping-zeng

139 Stanway, David. "Explainer: China's Mojiang Mine and Its Role in the Origins of COVID-19." *Reuters,* 9 June 2021, www.reuters.com/business/healthcare-pharmaceuticals/chinas-mojiang-mine-its-role-origins-covid-19-2021-06-09/.

140 Qiu, Jane. "How China's 'Bat Woman' Hunted Down Viruses from SARS to the New Coronavirus." *Scientific American*, 1 June 2020, www.scientificamerican.com/article/how-chinas-bat-woman-hunted-down-viruses-from-sars-to-the-new-coronavirus1/

ID4991 vs. RaTG13: SARS-CoV-2's "Closest Relative"

A 2016 paper published by PRC researchers (most of whom are affiliated with the WIV) describes these efforts as researchers conducting "surveillance of coronaviruses in bats in an abandoned mineshaft in Mojiang County, Yunnan Province, China, from 2012–2013."[141] Shi and Hu are listed as coauthors. WIV researchers identified two new betacoronaviruses – HiBtCoV/3740-2 and RaBtCoV/4991. The study concluded, "RaBtCoV/4991 showed more divergence from human SARS-CoV than other bat SL-CoVs and could be considered as a new strain of this virus lineage."[142] Shi designed and coordinated the study, drafted the manuscript, and is listed as the corresponding author.

Four years later and after the initial reports of an unknown SARS-like coronavirus in Wuhan, Shi and 28 other PRC scientists submitted an article to *Nature* for publication entitled, "A pneumonia outbreak associated with a new coronavirus of probably bat origin,"[143] on January 20, 2020. It was published in early February. It should be noted that this manuscript was submitted on the same day the PRC's National Health Commission first issued a statement confirming human-to-human transmission – one month after local health officials warned the CCP human-to-human transmissions were occurring.[144] It is highly unlikely Shi and her coauthors would have written this paper the same day they submitted it, meaning they were aware for days or perhaps weeks that the virus was spreading via from human-to-human transmission and did not alert the world. According to a study by researchers at the University of Southampton, implementing appropriate restrictions based on human-to-human transmission just one week before this paper was published would have reduced the number of cases in Wuhan by 66%.[145] This would have made a significant difference in the spread of the virus, especially in conjunction with the significant travel that occurred during the Spring Festival, which ran from January 10 to January 23, 2020, when the city of Wuhan was locked down.

Shi is listed as the corresponding author for the article, which states that COVID-19 "has now progressed to be transmitted by human-to-human contact."[146] The researchers conclude that RaTG13, an allegedly naturally occurring bat coronavirus, is the closest relative to SARS-CoV-2 (emphasis added):

> **We then found that a short region of RNA-dependent RNA polymerase (RdRp) from a bat coronavirus (BatCoV RaTG13)**—which was previously detected in Rhinolophus affinis from Yunnan province—showed high sequence identity to 2019-nCoV. **We carried out full-length sequencing** on this RNA sample (GISAID accession number EPI_ISL_402131). Simplot analysis showed that 2019-nCoV was highly similar throughout the genome to RaTG13 (Fig. 1c), with an overall genome sequence identity of 96.2%. Using the aligned genome sequences of 2019-nCoV, RaTG13, SARS-CoV and previously reported bat SARSr-CoVs, no evidence for recombination events was detected

141 Ge, Xing-Yi et al. "Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft." *Virologica Sinica,* 3 Feb. 2016; 31(1): 31-40. https://dx.doi.org/10.1007%2Fs12250-016-3713-9

142 Ibid.

143 Zhou, P., et al. "A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 3 Feb 2020, 579: 270–273. https://doi.org/10.1038/s41586-020-2012-7

144 Wang, Yanan. "Human-to-Human Transmission Confirmed in China Coronavirus." *AP NEWS*, 20 Jan. 2020. https://apnews.com/14d7dcffa205d9022fa9ea593bb2a8c5

145 Lai, Shengjie, et al. "Effect of Non-Pharmaceutical Interventions for Containing the COVID-19 Outbreak in China." *MedRxiv*, 2020, https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v3.

146 Zhou (2020).

> in the genome of 2019-nCoV. Phylogenetic analysis of the full-length genome and the gene sequences of RdRp and spike (S) showed that—for all sequences—**RaTG13 is the closest relative of 2019-nCoV and they form a distinct lineage from other SARSr-CoVs** (Fig. 1d and Extended Data Fig. 2)…**The close phylogenetic relationship to RaTG13 provides evidence that 2019-nCoV may have originated in bats.**[147]

A close examination of the paper, and the corrections published months later, reveal inconsistences in the researchers' claims. Several of the statements made in the above quotation are simply false. After months of criticism and questioning about RaTG13, Shi and the other researchers were forced to publish an addendum on November 17, 2020. **That addendum reveals that RaTG13 was actually ID4991, the sample collected years prior in 2012 or 2013, and that the full-length genomic sequence was obtained in 2018, not in January 2020 as the paper originally stated.**[148]

Unfortunately, no other labs can confirm the genomic sequence of RaTG13 – Shi said in an interview published in *Science Magazine* that the entire sample was used up after genomic sequencing.[149] The inability of outside researchers to verify the genome of RaTG13, and the above efforts to obfuscate when the WIV collected and sequenced RaTG13, raises multiple questions:

- Why leave out of the February 2020 article that the virus sequence was renamed?
- Why lie about when the full-length sequence was obtained?
- Why only issue a correction almost ten months later?
- Why was this sample destroyed via testing when others weren't?

In December 2020, reporters from *BBC News* attempted to visit the cave in Yunnan where RaTG13 was collected. They found themselves followed by plain-clothes police officers and stopped at checkpoints where they were told to stay out of the area.[150] A French publication, *Envoye Special*, produced a video in which they reported conversations with villagers who lived near the mine. According to one of those villagers, the mine was closed and monitored via surveillance cameras. That villager also alleged several people were arrested for venturing too close to the mine.[151]

It is important to note that in March 2020, American, British, and Australian researchers published "The proximal origin of SARS-CoV-2" in *Nature Magazine*.[152] Regarding RaTG13, they found, "Although RaTG13, sampled from a Rhinolophus affinis bat, is ~96% identical overall to SARS-CoV-2, its spike diverges in the RBD, which suggests that it may not bind efficiently to human ACE2."[153] "RBD" is an abbreviation for receptor-binding domain, part of the virus' spike protein. **This is the same part of the virus' genome that Shi, Hu, and other WIV researchers were genetically modifying and replacing as far back as 2015.**

147 *Ibid.*

148 Zhou, P., et. al. "Addendum: A pneumonia outbreak associated with a new coronavirus of probable bat origin." *Nature*, 17 Nov. 2020, 588: E6. https://doi.org/10.1038/s41586-020-2951-z

149 Shi, Zheng-li. "Reply to Science Magazine." *Science Magazine,* https://www.sciencemag.org/sites/default/files/Shi%20Zhengli%20Q%26A.pdf

150 Sudworth, John. "Covid: Wuhan Scientist Would 'Welcome' Visit Probing Lab Leak Theory." *BBC News,* 21 Dec. 2020, www.bbc.com/news/world-asia-china-55364445.

151 Asis, Francisco de. "Quite Important the Conversation with Danaoshan Inhabitant.- He Pointed towards the Location We Already Knew for the Mine.- The Roadblocks Are Probably the Diverted Traffic We Already Observed Too.Rest of the Story Is Just Incredible! Pic.twitter.com/kzHz7v5rSg." *Twitter,* Twitter, 12 Mar. 2021, https://twitter.com/franciscodeasis/status/1370183826731888641?s=20.

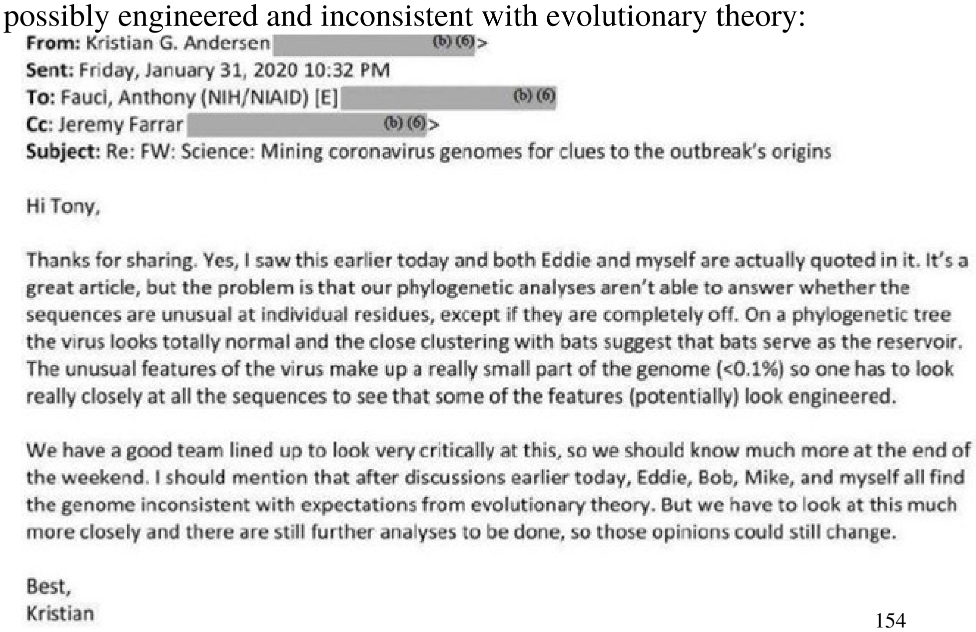
152 Andersen, Kristian G et al. "The proximal origin of SARS-CoV-2." *Nature Medicine,* 17 March 2002, 26(4):450-452. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7095063/

153 I*bid.*

If SARS-CoV-2 was genetically modified, this could represent a viable model for how. RaTG13's RBD, or full spike protein, could be replaced using the WIV's reverse genetic system. If one of the many unpublished coronaviruses in the WIV's possession was modified, and the resulting chimeric virus was then exposed to hACE2 expressing mice or civets, the resulting virus could become better adapted to infecting humans – just like SARS-CoV-2.

According to scientists – including those working at the WIV – ID4991/RaTG13 is more closely related to SARS-CoV-2 than any other publicly identified virus. It's now clear WIV researchers had this virus as early as 2013, several years before the WIV began genetically modifying other coronaviruses found in the wild. **Given the largest difference between RaTG13 and SARS-CoV-2 is at the spike protein – precisely where the WIV modified various coronaviruses for years – and that WIV researchers renamed the virus and lied about when they sequenced, ID4991/RaTG13 could be a source of genetic material if SARS-CoV-2 was indeed genetically modified.**

According to emails obtained by *Buzzfeed News,* it appears Kristian G. Andersen, the lead and corresponding author of the abovementioned article, initially considered this a viable theory. In a January 31, 2020 email to Dr. Anthony Fauci, the director of NIAID, Andersen stated that parts of the virus were possibly engineered and inconsistent with evolutionary theory:



From: Kristian G. Andersen [redacted] (b) (6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6)
Cc: Jeremy Farrar [redacted] (b) (6)>
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

[154]

Fig. 8: Andersen Email Suggesting SARS-CoV-2 was Genetically Modified

The WIV's intentionally misleading February 2020 paper regarding RaTG13 was uploaded as a preprint on January 23rd.[155] Given that Andersen and his coauthors cited it in their March 2020 paper, it is all but certain that Andersen, Dr. Fauci, and the others would have seen it before Andersen sent this email. The day after Anderson emailed Dr. Fauci on February 1, 2020, Dr. Fauci, Andersen, and others debated this issue via teleconference. Previously, they had agreed to keep the debate confidential. Following this discussion, Andersen abandoned his claims that the virus was genetically modified.[156] It is unclear what was said on this call that led to Anderson doing so.

154 Andersen, Kristian G. Email to Anthony Facui and Jeremy Farrar. 31 Jan. 2020. https://s3.documentcloud.org/documents/20793561/leopold-nih-foia-anthony-fauci-emails.pdf

155 Zhou, Peng, et. al. Preprint of "Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin." 23 Jan. 2020, *bioRxiv*, https://www.biorxiv.org/content/10.1101/2020.01.22.914952v2

156 Young, Alison. "'I Remember It Very Well': Dr. Fauci Describes a Secret 2020 Meeting to Talk about COVID Origins." *USA Today*, 18 June 2021, www.usatoday.com/story/opinion/2021/06/17/covid-19-fauci-lab-leaks-wuhan-china-origins/7737494002/.

Additional Cover-Up Activities by Scientists at the WIV

As more investigative work continues on the type of research being conducted at the WIV, CCP censors and WIV researchers have been deleting or scrubbing references to coronavirus research that could be related to the origins of the COVID-19 pandemic. As previously discussed, Ben Hu received a Youth Science Fund Project award to test the pathogenicity of two novel SARS-related coronaviruses beginning in 2019. In some publicly facing PRC websites, Hu's name has now been struck from the grant.

C010802	To study the mechanism of baculovirus Ac34 protein inhibiting the nuclear pathway of mammalian CRM1	Mu Jingfang	Wuhan Institute of Virology, Chinese Academy of Sciences
C010802	Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2		Wuhan Institute of Virology, Chinese Academy of Sciences
H1904	Study on the mechanism of enterovirus 71 type 3A protein antagonizing RNAi antiviral immunity	Qiu Yang	Wuhan Institute of Virology, Chinese Academy of Sciences

Fig. 9: Ben Hu's Name Removed From 2019 Grant [157]

Of the almost 80 WIV grants listed in the database, the one awarded to Ben Hu is the only one that does not identify the principal investigator.

A December 12, 2017, interview with Hu was pulled offline after it began circulating on Twitter. In the article, Hu discusses monitoring and collecting samples from the bat cave in Yunnan and his work using the reverse genetic system to insert spike proteins into live coronaviruses. Interestingly, he discusses how Shi Zheng-li "often personally leads the team to take samples."[158] It is likely that this article was pulled down for drawing attention to the cave where RaTG13 was collected.

Similarly, a 2018 article written by Hu and published on the website for the Wuhan Branch of the Chinese Academy of Sciences has also been removed.[159] While the article broadly discusses the work of Shi and other researchers at the WIV, it does not offer any unique insight or evidence of dangerous research. So why was it removed?

157 2019 Natural Science Foundation Query and Analysis System. https://journal.medsci.cn/m/nsfc.do?u=%E4%B8%AD%E5%9B%BD%E7%A7%91%E5%AD%A6%E9%99%A2%E6%AD%A6%E6%B1%89%E7%97%85%E6%AF%92%E7%A0%94%E7%A9%B6%E6%89%80

158 "Hunting bat viruses, tracking the origin of SARS, an interview with Dr. Hu Ben, Wuhan Institute of Virology, Chinese Academy of Sciences." *First Author,* 12 Dec. 2017, https://archive.vn/sVHmq#selection-45.79-45.215

159 Hu, Ben. "The Wuhan Institute of Virology's "Research on Chinese Bats Carrying Important Viruses" won the first prize of the 2018 Hubei Provincial Natural Science Award." *Wuhan Branch, Chinese Academy of Sciences, 13* April 2018, archived: https://web.archive.org/web/20210107222832/http://whb.ac.cn/xw/kyjz/201811/t20181122_5191050.html

Perhaps most incriminating are Shi's repeated lies about activities taking place at the WIV. In August 2020, after the publication of the Committee Minority Staff's interim report, the China Global Television Network interviewed Shi about our work. In the resulting article, Shi denied that Major General Chen Wei took over the BSL-4 lab:

> Liu Xin: The report actually went further and said that the lab has been taken over by the Chinese military. It says that Major General Chen Wei has succeeded Yuan Zhiming as the Director of the WIV and Chen Wei is a Chinese military medical sciences expert.
> Shi Zhengli: This is a rumor; there is no such thing.
> Liu Xin: You absolutely deny that the Chinese military has taken over the WIV.
> Shi Zhengli: Yes, it is a rumor.[160]

This is demonstrably false. As previously discussed, posts made on CCP-controlled forums announcing Chen's arrival acknowledged her takeover of the lab. The report stated, "PLA Maj. Gen. Chen Wei has been in Wuhan for more than 10 days. She took over the P4 lab as if it were a 'reassurance pill.'"[161]

During the same interview, and in response to Committee Minority Staff raising questions about a possible lab leak, Shi again lied, claiming that all of the WIV's research has been published and their samples available for review:

> Another piece of evidence that I can give you is that our lab has been doing research for 15 years, and all our work has been published. We also have a library of our own genetic sequences, and we have experimental records of all our work related to the virus, which are accessible for people to check.[162]

This, again, is demonstrably false. The WIV's sequence library was taken offline in September 2019 and is not "accessible for people to check." Given the previously discussed undisclosed coronavirus research and military activities at the WIV, it is obvious that not "all" of the WIV's work has been published. Daszak confirmed this in an interview with *Nature*: "we have data that we've gathered over 15 years of working in China — 5 years under a previous grant from the NIH — which haven't been published yet."[163]

In a June 2021 interview, Shi told the *New York Times*, "my lab has never conducted or cooperated in conducting GOF experiments that enhance the virulence of viruses."[164] This is a bizarre claim given the years of published research, often designed and led by Shi, that explicitly sought to make coronaviruses more infectious to humans. In the same interview, Shi lied about WIV researchers falling ill in the fall of 2019 – "The Wuhan Institute of Virology has not come across such cases." This is despite the State Department's January 15th 2021 fact sheet and confirmation from a Dutch virologist on the WHO's investigative team that several researchers were sick.[165]

160 Xin, Liu. "Exclusive Interview: CGTN's Liu Xin Talks to China's 'Bat Woman'." *CGTN*, 26 Aug. 2020, https://news.cgtn.com/news/2020-08-22/Can-politics-be-put-aside-while-looking-for-origins-of-coronavirus--T9HgctyKv6/index.html.

161 Guli.

162 Xin.

163 Subbaraman, Nidhi. "'Heinous!': Coronavirus Researcher Shut down for Wuhan-Lab Link Slams New Funding Restrictions." *Nature News,* 21 Aug. 2020, www.nature.com/articles/d41586-020-02473-4.

164 Qin, Amy, and Chris Buckley. "A Top Virologist in China, at Center of a Pandemic Storm, Speaks Out." *The New York Times,* 14 June 2021, www.nytimes.com/2021/06/14/world/asia/china-covid-wuhan-lab-leak.html

165 Gordon, Michael R., et al. "WSJ News Exclusive | Intelligence on Sick Staff at Wuhan Lab Fuels Debate on Covid-19 Origin." *The Wall Street Journal,* 23 May 2021, www.wsj.com/articles/intelligence-on-sick-staff-at-wuhan-lab-fuels-debate-on-covid-19-origin-11621796228.

Cover-Up Activities by the Chinese Communist Party

According to a WHO internal document from August 2020, the PRC put little effort into determining the source of the SARS-CoV-2 after January 2020:

> Following extensive discussions with and presentation from Chinese counterparts, it appears that little had been done in terms of epidemiological investigations around Wuhan since January 2020. The data presented orally gave a few more details than what was presented at the emergency committee meetings in January 2020. No PowerPoint presentations were made and no documents were shared.[166]

Given the large amount of financial resources devoted by the PRC in the years prior for locating, sampling, identifying, and experimenting with coronaviruses, it is odd that little effort would be put into determining the source of the virus, if the source was unknown. In mid-February 2020, the PRC's Ministry of Science and Technology issued new guidelines for laboratory research in the PRC. Official PRC sources stressed:

> The mention of biosafety at labs by the ministry has nothing to do with some saying that the coronavirus leaked from the Wuhan Institute of Virology of the Chinese Academy of Sciences.[167]

Experts interviewed in February 2020 by *The Global Times* stated that PRC labs paid "insufficient attention to biological disposal."[168] This included disposing of lab materials into sewage systems.[169] Given that these new guidelines were issued after the PRC stopped searching for the source of the outbreak, it raises questions as to what prompted the PRC to stop its search.

Shortly thereafter, on February 25, 2020, the Chinese Center for Disease Control and Prevention issued supplementary regulations affecting how PRC scientists work on research related to COVID-19. The guidelines prohibit researchers from sharing data or samples and requires them to receive permission prior to conducting research or publishing the results.

> 3. No one can, under their own name or in the name of their research team, provide other institutions and individuals with information related to the COVID-19 epidemic on their own, including data, biological specimens, pathogens, culture, etc.
>
> 4. Before publishing papers and research results related to the COVID-19 epidemic, you must first report them to the Science and Technology Group/Department for preliminary review, and if necessary, submit it to the Emergency Leading Group or the Department of Science and Education of the National Health Commission for approval.
>
> Papers that have been submitted but not yet reviewed by the Science and Technology Group/Department should be withdrawn as soon as possible and redone according to these regulations.

Fig. 10: Excerpt from China CDC Regulations Issued on February 25th [170]

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166 Kirchgaessner, Stephanie. "China Did 'Little' to Hunt for Covid Origins in Early Months, Says WHO Document." *The Guardian,* 23 Feb. 2021, www.theguardian.com/world/2021/feb/23/china-did-little-hunt-covid-origins-early-months-says-who-document

167 Caiyu, Liu, and Leng Shumei. "Biosafety Guideline Issued to Fix Chronic Management Loopholes at Virus Labs." *Global Times,* 16 Feb. 2020, www.globaltimes.cn/content/1179747.shtml.

168 *Ibid.*

169 *Ibid.*

A full copy of the regulations is included in the Appendix.

On February 27, 2020, *Health Times,* published remarks from an interview with Yu Chuanhua, who referenced health data from February 25th. Yu is the Vice President of the Hubei Health Statistics and Information Society and Professor of Epidemiology and Health Statistics at Wuhan University, and was running a database of confirmed COVID-19 cases in early 2020. In the interview, Yu stated he had evidence of COVID-19 cases as early as September 2019:

> Professor Yu Chuanhua said, "For example, there is data on a patient who became ill on September 29. The data shows that the patient has not undergone nucleic acid testing. The clinical diagnosis (CT diagnosis) is a suspected case. The patient has died. This data has not been confirmed and there is no time to death. It may also be wrong data." With the research of the database, Professor Yu Chuanhua found more and more case data before December 8. There were two cases in November, and the onset time was November 14 and November 21, 2019. Before December 8, there were also five or six cases. Among them, one patient who became ill at the end of November was hospitalized on December 2 and was clinically diagnosed with pneumonia.[171]

Before the interview was published on February 27th, Yu called the reporter and tried to retract the information regarding the two sick patients in November.[172] It is likely that this was done to comply with the China CDC gag order that was issued two days prior.

Nine days later, on March 5, 2020, the Joint Prevention and Control Mechanism (JPCM) of the State Council Novel Coronavirus Pneumonia Scientific Research Group issued a confidential memo, obtained by the *Associated Press*, entitled, "Notice on the Standardization of the Management and Publication of Novel Coronavirus Scientific Research."[173] The notice announced the research group was taking control of all publication work related to the pandemic for "coordinated deployment."[174] It also required units publishing research to notify the JPCM's propaganda team, which was tasked to work with a special public opinion team to coordinate publication of research with public opinion and "social concerns."[175]

170 Chinese Center for Disease Control and Prevention. "On the Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus." 25 Feb. 2020. https://www.documentcloud.org/documents/7340336-China-CDC-Sup-Regs.html

171 Wang, Zhenya. "Experts Judge the Source of the New Crown: December 8 Last Year May Not Be the Earliest Time of Onset." *Health Times,* 27 Feb. 2020, www.jksb.com.cn/index.php?m=wap&a=show&catid=629&id=160018.

172 *Ibid.*

173 Joint Prevention and Control Mechanism of the State Council Novel Coronavirus Pneumonia Scientific Research Group. "Notice on the Standardization of the Management and Publication of Novel Coronavirus Scientific Research." 3 Mar. 2020. https://www.documentcloud.org/documents/7340337-State-Research-regulations.html

174 *Ibid.*

175 *Ibid.*

Each member work unit of the scientific research team will gather scientific research information within their own unit and systems, review and check the content and form of its publication, and report it to the scientific research team for approval in a timely manner. The scientific research group's dedicated teams of professionals and various experts are responsible for reviewing the publication's content and format and giving expert opinions, and when necessary, arranging expert assessment. After the scientific research group approves, the publishing work unit should, according to work requirements, arrange publication via press conferences, official websites, state social media, news media and other platforms, and notify the propaganda and scientific research teams of the Joint Prevention and Control Mechanism of the State Council. In principle, COVID-19 scientific research should be published first in the form of an official authoritative publication. The special group on public opinion should strengthen communication with the propaganda team, take into account the trend of public opinion and social concerns, and strengthen guidance of the publication of scientific research and information.

Fig. 11: Excerpt from JPCM Memo

The memo concludes with a warning: "Those who fail to apply for approval in accordance with the prescribed procedures and publish unconfirmed false information on scientific research, thereby causing serious adverse social impacts, shall be held accountable."[176] A full copy of the memo is included in the Appendix. These documents are clear evidence of the CCP's effort to restrict research on SARS-CoV-2, so that the only research published supports the Party's official story on the origins and emergence of COVID-19.

After the release of the Committee Minority Staff's interim report on the origins of COVID-19, *China Global Television Network*, a PRC state-owned media outlet, released a propaganda video aimed at undermining this investigation. Entitled, "Clearing up confusion in McCaul report on COVID-19," the approximately 45-minute video labels the report "misinformation."[177] It also discusses what they call the "tired old theory that the virus could have leaked from a lab"[178] and reveals that Shi Zheng-li was interviewed about our report. The piece also claims the BSL-4 lab space at the WIV was never taken over by Maj. Gen. Chen Wei.[180] As discussed earlier, this statement is demonstrably untrue.

In June 2021, Jesse Bloom published a preprint entitled, "Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic." Bloom is a Principal Investigator and Associate Professor for Basic Sciences and the Herbold Computational Biology Program at Fred Hutch, a cancer research center. Bloom was able to recover multiple deleted viral sequences collected from patients in Wuhan in early December 2020. These sequences were originally uploaded to the NIH's Sequence Read Archive by researchers in Wuhan, but later deleted at their request.

176 *Ibid.*

177 "The Point: Clearing up Confusion in the McCaul Report On Covid-19." *CCTV News*, 25 July 2020, www.youtube.com/watch?v=n5qYogMTZOw.

178 *Ibid.*

179 *Ibid.*

180 *Ibid.*

Oddly, these samples more greatly diverge from SARS-CoV-2's bat coronavirus ancestor – "the earliest SARSCoV-2 sequences were collected in Wuhan in December, but these sequences are more distant from RaTG13 than sequences collected in January from other locations in China or even other countries."[181] Bloom concludes (emphasis added):

> **The fact that this informative data set was deleted suggests implications beyond those gleaned directly from the recovered sequences.** Samples from early outpatients in Wuhan are a gold mine for anyone seeking to understand spread of the virus. Even my analysis of 13 partial sequences is revealing, and it clearly would have been more scientifically informative to fully sequence all 34 samples rather than delete the partial sequence data. **There is no obvious scientific reason for the deletion:** the sequences are concordant with the samples described in Wang et al. (2020a,b), there are no corrections to the paper, the paper states human subjects approval was obtained, and the sequencing shows no evidence of plasmid or sample-to-sample contamination…. Even though the sequencing data were on the Google Cloud (as described above) and the mutations were listed in a table in the Small paper by Wang et al. (2020b), **the practical consequence of removing the data from the SRA was that nobody was aware these sequences existed.** Particularly in light of the directive that labs destroy early samples (Pingui 2020) and multiple orders requiring approval of publications on COVID-19 (China CDC 2020; Kang et al. 2020a), **this suggests a less than wholehearted effort to maximize information about viral sequences from early in the Wuhan epidemic.**[182]

The PRC's efforts to obfuscate the origins of COVID-19 were not limited to destroying samples and silencing doctors, but featured a sustained disinformation campaign as well. As discussed in our previous report, Lijian Zhao, an official within the PRC's Foreign Ministry, shared an article on Twitter that claimed the virus was brought to the PRC by the U.S. military.[183] The article was from the *Global Times* research.ca, a website that pushes pro-Putin propaganda and has reported ties to Russian state media.[184] His tweet was amplified by the Chinese Embassy in South Africa.[185]

181 Bloom, Jesse D. Preprint: "Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic." *bioRxiv*, 29 June 2021, https://www.biorxiv.org/content/10.1101/2021.06.18.449051v2

182 *Ibid.*

183 Zhao, Lijian. "This Article Is Very Much Important to Each and Every One of Us. Please Read and Retweet It. COVID-19: Further Evidence That the Virus Originated in the US. Https://T.co/LPanIo40MR." *Twitter*, 13 Mar. 2020, www.twitter.com/zlj517/status/1238269193427906560

184 Thomas, Elise, and Aspi. "Chinese Diplomats and Western Fringe Media Outlets Push the Same Coronavirus Conspiracies." *The Strategist,* 30 Mar. 2020, www.aspistrategist.org.au/chinese-diplomats-and-western-fringe-media-outlets-push-the-same-coronavirus-conspiracies/.

185 Chinese Embassy in South Africa. "More Evidence Suggests That the Virus Was Not Originated at the Seafood Market in Wuhan at All, Not to Mention the so Called 'Made in China'. Https://T.co/8cRxkSZB3z." *Twitter*, 16 Mar. 2020, www.twitter.com/ChineseEmbSA/status/1239453193689587712



Fig. 12: PRC Spokesman Tweet Suggesting COVID-19 Arrived in Wuhan via the Military World Games

To further drive this narrative, CCP-controlled media outlets accused Maatje Benassi, a member of the U.S. Army Reserve, as being "patient zero." Benassi competed at the Military World Games without becoming ill, yet has been repeatedly targeted for harassment. Videos pushing the theory have been uploaded to WeChat, Weibo, and Xigua – PRC based sites. Two weeks after Zhao tweeted that the U.S. army brought the virus to Wuhan, the *Global Times* amplified the narrative, urging the U.S. government to release athletes' health info and repeated the claim about Benassi. [186]

Another tweet by Zhao actually suggests the pandemic did start in September, as is suggested in this addendum, but that it began in the United States.[187]



Fig. 13: PRC Spokesman Tweet Suggesting the COVID-19 Pandemic Started in September 2019.

186 Shumei, Leng, and Wan Lin. "US Urged to Release Health Info of Military Athletes Who Came to Wuhan in October 2019." *Global Times,* 25 Mar. 2020, www.globaltimes.cn/content/1183658.shtml.

187 Zhao, Lijian. *US CDC Admitted Some #COVID19 Patients Were Misdiagnosed as Flu during 2019 Flu Season. 34 Million Infected & 20000 Died. If #COVID19 Began Last September, & US Has Been Lack of Testing Ability, How Many Would Have Been Infected? US Should Find out When Patient Zero Appeared.* Twitter, 22 Mar. 2020, https://twitter.com/zlj517/status/1241723635964039168?s=20.

It is important to note that this tweet was sent in March 2020. The previously discussed Harvard study suggesting the pandemic began in September was not published until the second half of 2020. This accusation came ten days after Zhao repeated his theory that the U.S. military brought COVID-19 to Wuhan. If the CCP realized an investigation would show an uptick in visits of patients with symptoms similar to COVID-19 in September, October, and November of 2019, this would likely be the actions they would take to coverup the source of those illnesses.

WIV Disinformation Campaign Involving Peter Daszak

As we have previously explained, Peter Daszak was heavily involved in the gain-of-function research taking place at the WIV, including research that was done at BSL-2 levels and that was done while the United States had a moratorium in place on funding gain-of-function research. In addition, we have uncovered strong evidence that suggests Peter Daszak is the public face of a CCP disinformation campaign designed to suppress public discussion about a potential lab leak. Emails obtained by a third-party organization show that Daszak organized a February 19, 2020, statement in the *Lancet* "condemn[ing] conspiracy theories suggesting that COVID-19 does not have a natural origin."[188] The statement continued, "Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus."[189] The emails show Daszak's effort to organize a large group of scientists to sign onto a statement that he personally drafted. One email concludes with Daszak stating, "Please note that this statement will not have EcoHealth Alliance logo on it and will not be identifiable as coming from any one organization or person, the idea is to have this as a community supporting our colleagues."[190]

The emails, sent from Daszak's EcoHealth Alliance email account, also reveal the statement was drafted in response to a request by WIV researchers with whom Daszak had worked (emphasis added):

> You should know that the conspiracy theorists have been very active, targeting our collaborators with some extremely unpleasant web pages in China, and some have now received death threats to themselves and their families. **They have asked for any show of support we can give them.**[191]

In a separate email, Daszak states that Linfa Wang (who did not sign the statement) pushed for Daszak and Baric to not sign the statement, effectively hiding their involvement. As previously discussed, Linfa Wang, who is copied on several other emails about the statement, was a coauthor of multiple Daszak/Shi/Hu papers. Wang is currently the Director and Professor of the Program in Emerging Infectious Diseases at the Duke-NUS Graduate Medical School in Singapore. He is a PRC national who received his B.S. in biochemistry from the East China Normal University in Shanghai, PRC[192] before completing a Ph.D. in molecular biology at the University of California, Davis in the United States.

188 Calisher, Charles et al. "Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19." *Lancet*, 7 Mar. 2020, 395(10226): e42-e43. https://pubmed.ncbi.nlm.nih.gov/32087122/

189 *Ibid.*

190 Daszak, Peter. Email to Linda Saif, Hume Field, JM Hughe, Rita Colweel, Alison Andrew, Aleksei Chmura, Hongying Li, William B. Karesh, and Robert Kessler. 6 Feb. 2020. https://usrtk.org/wp-content/uploads/2020/11/The_Lancet_Emails_Daszak-2.6.20.pdf

191 Daszak, Peter. Email to Rita Colwell. 8 Feb. 2020. https://usrtk.org/wp-content/uploads/2020/11/The_Lancet_Emails_Daszak-2.8.20.pdf

192 Wang, Linfa. "Curicullum Vitae." https://globalhealth.duke.edu/sites/default/files/cv/cv-linfa_wang-jan2017.pdf

In January 2020, Wang was at the WIV in Wuhan, visiting researchers he worked with. Given his previous publications, this likely included a vsiit with Hu and Shi, with whom he has authored dozens of papers. He departed the city on January 18th,[192] less than three weeks before Daszak externally circulated his draft *Lancet* statement. Wang is included on the email soliciting cosigners.[193]

In the email, Daszak states, (emphasis added):

> I spoke with Linfa last night about the statement we sent round. He thinks, and I agree with him, that **you, me and him should not sign this statement, so it has some distance from us** and therefore doesn't work in a counterproductive way... **We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice.**[194]

Copies of these emails are included in the Appendix.

While pushing for Daszak and Baric, the WIV's most prominent American collaborators, to hide their efforts to organize this statement, Wang was serving as the Chair of the Scientific Advisory Board for the Center for Emerging Diseases at the Wuhan Institute of Virology, of which Shi Zheng-li is the Director.[195]

Baric agreed and chose not to sign. It is unclear why Daszak ultimately changed his mind and signed the statement. Despite Daszak's role as the organizer of the *Lancet* statement, Charles Calisher is listed as the corresponding author. Oddly, the email address listed for Calisher is a generic one (COVID19statement@gmail.com[196]) that appears to have been created specifically for this statement, an unusual practice for scientific publications.

The February 2021 Lancet statement declared the authors had "no competing interest," despite Daszak organizing the letter on behalf of WIV researchers who he funded and with whom he collaborated. In June 2020, after public concerns regarding Daszak's connection to the WIV, "the *Lancet* invited the 27 authors of the letter to re-evaluate their competing interests."[197] **Daszak submitted a revised disclosure statement which, while transparent about his prior work with PRC researchers, fails to reference the WIV or disclose that he drafted the statement at the request of PRC researchers**.[198]

The emails also reveal that Daszak helped edit a letter sent on February 6, 2020 by the Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine to the White House Office of Science and Technology Policy regarding the origins of COVID-19.

192 Kupferschmidt, Kai. "This Biologist Helped Trace SARS to Bats. Now, He's Working to Uncover the Origins of COVID-19." Science, 9 Sept. 2020, www.sciencemag.org/news/2020/09/biologist-helped-trace-sars-bats-now-hes-working-uncover-origins-covid-19.

193 Daszak (6 Feb.)

194 Daszak, Peter. Email to Ralph Baric, Toni Baric, Alison Andre, and Aleksei Chmura. 6 Feb. 2020. https://usrtk.org/wp-content/uploads/2021/02/Baric_Daszak_email.pdf

195 Wang.

196 Calisher.

197 Editors of The Lancet. "Addendum: competing interests and the origins of SARS-CoV-2." *The Lancet,* 26 June 2021, 397: 2449-50. https://www.thelancet.com/action/showPdf?pii=S0140-6736%2821%2901377-5

198 *Ibid.*

199 McNutt, Marcia, et al. "NASEM Response to OSTP Re Coronavirus_February 6, 2020." Received by Kelvin Droegemeier , National Academies of Science, Engineering, and Medicine, 6 Feb. 2020, Washington, District of Columbia. https://www.nationalacademies.org/documents/link/LDA8FF8BAB7F1D4A98AC250C7916649E610A15AD51C6/fileview/DA215521A660F40FD8D752FFB82A8E21FA8D3C29976D/NASEM%20Response%20to%20OSTP%20re%20Coronavirus_February%206%2C%202020.pdf?hide=thumbs+breadcrumbs+favs+props+nextprev+sidebar+pin+actions&scheme=light&fitwidth

While not included in the final version, the last draft edited by Daszak and the other experts who were consulted included a line stating, "The initial views of the experts is that the available genomic data are consistent with natural evolution and that there is currently no evidence that the virus was engineered to spread more quickly among humans." Daszak actually pushed for broader language, as he believed "this is a bit too specific, because there are other conspiracy theories out there." It is unclear why the sentence was removed by the Presidents of the U.S. National Academies before the letter was sent to the White House. Daszak specifically sought to time the publication of his statement in The Lancet for after this letter was released. And the statement references the letter as proof of the virus' natural origin, without disclosing that Daszak helped edit it. It is highly likely that senior government officials, including Dr. Fauci, would have seen both the letter from the U.S. National Academies of Sciences, Engineering, and Medicine and the statement published in The Lancet, shaping their opinion and stifling debate within the U.S. federal government regarding the origins of COVID-19.

Sixteen months after sending this initial letter, the Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine released an updated statement on June 15, 2021, titled, "Let Scientific Evidence Determine Origin of SARS-CoV-2, Urge Presidents of the National Academies." [199] This updated statement acknowledges there are scenarios that the origin of the pandemic could have resulted from a lab leak, stating (emphasis added):

> However, misinformation, unsubstantiated claims, and personal attacks on scientists surrounding the different theories of how the virus emerged are unacceptable, and are sowing public confusion and risk undermining the public's trust in science and scientists, including those still leading efforts to bring the pandemic under control… In the case of SARS-CoV-2, there are multiple scenarios that could, in principle, explain its origin with varying degrees of plausibility based on our current understanding. **These scenarios range from natural zoonotic spillover (when a virus spreads from non-human animals to humans) to those that are associated with laboratory work.**[200]

Unlike the letter to the White House, this statement does not state which, if any, outside experts were consulted when drafting the statement.

Interestingly, three weeks later, in July 2021, Daszak and his colleagues released an update to their February 2020 statement with a very similar title: "Science, not speculation, is essential to determine how SARS-CoV-2 reached humans." The second statement was signed by 24 of the original 27 authors and reflects a major step back from those authors' original position (emphasis added):

200 *Ibid.*

Interestingly, three weeks later, in July 2021, Daszak and his colleagues released an update to their February 2020 statement with a very similar title: "Science, not speculation, is essential to determine how SARS-CoV-2 reached humans." The second statement was signed by 24 of the original 27 authors and reflects a major step back from those authors' original position (emphasis added):

> **The second intent of our original Correspondence was to express our working view that SARS-CoV-2 most likely originated in nature and not in a laboratory,** on the basis of early genetic analysis of the new virus and well-established evidence from previous emerging infectious diseases, including the coronaviruses that cause the common cold as well as the original SARS-CoV and MERS-CoV. **Opinions, however, are neither data nor conclusions.** Evidence obtained using the scientific method must inform our understanding and be the basis for interpretation of the available information.[201]

This is quite different from Daszak's words in the first border-line propaganda statement "condemn[ing] conspiracy theories suggesting that COVID-19 does not have a natural origin."[202] Despite this softening, the authors continue to accuse those who seek to investigate the lab leak hypothesis of being the source of the PRC's unwillingness to cooperate with an international investigation:

> Allegations and conjecture are of no help, as they do not facilitate access to information and objective assessment of the pathway from a bat virus to a human pathogen that might help to prevent a future pandemic. Recrimination has not, and will not, encourage international cooperation and collaboration.[203]

Whereas the first statement cited the letter from the Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine (which Daszak helped edit), the second cites the Presidents' statement released just weeks prior. This raises the question of whether Daszak, or any of the authors, assisted in drafting or editing the June 15th statement issues by the National Academies.

It should also be noted that Daszak was the only representative of the United States on the WHO-China Joint Study team in early 2021. The United States put forth a list of experts to be considered, none of whom were chosen. Daszak was not on that list but was nevertheless selected and approved by the CCP.[204] The annexes of the WHO's report on the origins of COVID-19, issued in March 2021, include multiple examples of CCP disinformation that have been repeated by Daszak. This include a discussion of "conspiracy theories,"[205] which include the lab leak hypothesis and questions regarding the possible genetically modified nature of SARS-CoV-2. It also refers to the WIV's sequence database that was taken offline as a "rumour about missing data."[206] This is similar language to that which Daszak used during his Chatham House interview – despite the database remaining offline.[207] Committee Minority Staff was unable to determine whether Daszak assisted in the drafting or editing of the WHO report.

201 Calisher, Charles H et al. "Science, not speculation, is essential to determine how SARS-CoV-2 reached humans." *Lancet*, 5 July 2021, 398:209-211. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8257054/

202 Calisher (Feb.)

203 Calisher (July)

204 Testimony from former senior U.S. official received by Committee Minority Staff.

205 Joint Report - ANNEXES.

206 *Ibid.*

207 *Ibid.*

Peter Daszak has taken several additional concerning actions in regard to the origins of COVID-19, including inexplicably lying about the work conducted by EcoHealth Alliance in the months following the emergence of SARS-CoV-2. In an August 21, 2020, interview with *Nature,* after the NIH suspended the grants he was using to fund research at the WIV, Daszak claimed "The grant isn't used to fund work on SARS-CoV-2. Our organization has not actually published any data on SARS-CoV-2."[208] This is despite the fact that four days later Nature Communications published "Origin and cross-species transmission of bat coronaviruses in China."[209] Daszak, Shi, Hu, and Wang are all listed as authors, with Shi and Daszak both being listed as corresponding authors. The preprint for the article was uploaded on May 31, 2020, almost three months before Daszak's interview with *Nature*. The paper includes a phylogenetic analysis "suggesting a likely origin for SARS-CoV-2 in Rhinolophus spp. bats."[210] Daszak, Shi, three EcoHealth Alliance affiliated researchers, and Linfa Wang are credited with designing the study, conducting fieldwork, and establishing collection and testing protocols.

The research was funded by the NIH (grant no. R01AI110964) and USAID's PREDICT project (cooperative agreement number GHN-A-OO-09-00010-00), as well as the Strategic Priority Research Program of the Chinese Academy of Sciences (grant no. XDB29010101) that Shi was directing. It also received support from the National Natural Science Foundation of China (grants no. 31770175 and 31830096). The paper notes:

> All work conducted by EcoHealth Alliance staff after April 24th 2020 was supported by generous funding from The Samuel Freeman Charitable Trust, Pamela Thye, The Wallace Fund, & an Anonymous Donor c/o Schwab Charitable.[211]

April 24th was the day the NIH terminated the project Understanding the Risk of Bat Coronavirus Emergence, which was funded under grant R01AI110964,[212] which is cited in the paper as funding this work.[213] The grant Daszak told Nature was not being used to fund work on SARS-CoV-2 is cited in a paper presenting research on SARS-CoV-2.

Earlier, in March 2020, Peter Daszak and two other EcoHealth Alliance affiliated researchers published "A strategy to prevent future epidemics similar to the 2019-nCoV outbreak."[214] While the paper lacked lab experimentation, it discussed SARS-CoV-2 and claimed that "wildlife trade has clearly played a role in the emergence of"[215] the virus. This work was also funded by the same NIH grant (grant no. R01AI110964), as well as the same cooperative agreement with USAID's PREDICT Project.

In December 2020, Daszak stated in a tweet that the suspension of the aforementioned NIH grant directly prevented him from accessing samples at the WIV. If the grant did not support EcoHealth Alliance's work on SARS-CoV-2, how could it be related to their inability to access SARS-CoV-2 samples?

208 Subbaraman.
209 Latinne, Alice et al. "Origin and cross-species transmission of bat coronaviruses in China." *Nature Communications,* 25 Aug. 2020, 11(1):4235, https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7447761/
210 *Ibid.*
211 *Ibid.*
212 Lauer, Michael. Email to Peter Daszak. 24 April 2020. https://www.sciencemag.org/sites/default/files/Lauer.Daszak.NIH%20grant%20killed.partial%20email%20transcripts.April%202020.pdf
213 Latinne
214 Daszak, Peter et al. "A strategy to prevent future epidemics similar to the 2019-nCoV outbreak." *Biosafety and Health,* March 2020, 2(1): 6-8. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7144510/
215 *Ibid.*

Why did Daszak claim the NIH grant "isn't used to fund work on SARS-CoV-2"[216] when his own published research and statements show that it was?

Another concerning example of Daszak's behavior comes from a March 10, 2021 discussion with Chatham House. In response to a question about the WIV taking down its viral sequence and sample database in September 2019 and whether the WHO investigative team requested to see the data, Peter Daszak stated (emphasis added):

> I asked the question in front of the whole team, both sides, while we were at the Wuhan Institute of Virology, about the **so-called missing database.** And what we were told, by Shi Zheng-li, was that there had been hacking attempts on it, about 3,000 hacking attempts, and they took down this excel spreadsheet-based database. Absolutely reasonable. **We did not ask to see the data,** and as you know, a lot of this work is work that has been conducted with EcoHealth Alliance, and I'm also part of those data, and **we do basically know what's in those databanks.** And I shared, **I gave a talk to both sides about the work we've done with the Wuhan Institute of Virology and explained what's there. There is no evidence of viruses closer to SARS-CoV-2 than RaTG13 in those databases. It's as simple as that.**[217]

This is a stunning claim given the database contained more than 22,000 samples and was inaccessible by anyone outside of the WIV after September 2019. It was physically impossible for Daszak to remotely access the database after the SARS-CoV-2 genome was released in January 2020 in order to compare the genome to samples in the database. **If not, given that no one outside of the WIV knew RaTG13 was closely related to SARS-CoV-2 prior to publication in February 2020, how could Daszak claim to know there is not a closer match in one of the 22,000 plus samples when he could not access the data? This raises the question of whether he has copy of the database.**

Daszak has also been, at best, incorrect about how the WIV handed RaTG13. In an April 21, 2020 interview with the *New York Times,* he stated (emphasis added):

> We found the closest relative to the current SARS-CoV-2 in a bat in China in 2013. **We sequenced a bit of the genome, and then it went in the freezer;** because it didn't look like SARS, we thought it was at a lower risk of emerging. With the Virome project, we could have sequenced the whole genome, discovered that it binds to human cells and upgraded the risk. And maybe then when we were designing vaccines for SARS, those could have targeted this one too, and we would have had something in the freezer ready to go if it emerged.[218]

This is, of course, untrue. Researchers at the WIV fully sequenced RaTG13's genome in 2018.[219] Either Daszak knew this was untrue, and lied to the *New York Times,* or he was being kept in the dark about the work being conducted at the WIV. If the later is true, it raises more questions about Daszak's March 2021 claim to know everything in the WIV's database that was taken offline.

216 Subbaraman.

217 "Sustaining the Response: Inside the WHO-China Mission." *Chatham House,* 10 March 2021, https://www.youtube.com/watch?v=GMIlEF58944&t=3249s.

218 Kahn, Jennifer. "How Scientists Could Stop the Next Pandemic Before It Starts." *The New York Times,* 21 Apr. 2020, www.nytimes.com/2020/04/21/magazine/pandemic-vaccine.html.

219 Zhou, (Nov. 2020).

V. HYPOTHESIS: A LAB LEAK THAT CAUSED A PANDEMIC

Having examined the evidenced discussed in this addendum, Committee Minority Staff has put together the following hypothesis that could reasonably represent what could have occurred in the early months of the COVID-19 pandemic.

In the months leading up to an accidental release of SARS-CoV-2, the hazardous waste treatment system at the WNBL was undergoing renovation. The central air conditioning system at one of the facilities needed to be renovated, which likely resulted in lower than ideal air circulation and enabling viral particles to remain suspended in the air longer. After the July 4, 2019 notice from the Ministry of Science and Technology, and prior to the September 30th deadline, researchers at the WIV were reviewing samples collected under grant 2013FY113500, held by Yuan Zhiming, the Director of the WNBL BSL-4.[220]

This is the same grant which funded:

- The 2013 paper reporting the first isolation of a live SARS-like coronavirus after sampling at the cave in Kunming.[221]
- The 2014 paper, which was the result of collecting 986 samples from 39 species of small mammals in Guangxi and Yunnan provinces.
- The 2016 paper, where a second live coronavirus was successfully isolated.
- The 2017 paper, where a third live SARS-like coronavirus was isolated and WIV researchers created eight chimeric coronaviruses with altered spike proteins.

Hu, Shi, and others at the WIV were actively testing novel and genetically manipulated coronaviruses against hACE2 expressing mice and civets at BSL-2 and BSL-3 conditions, including viruses collected from the cave in Yunnan where the miners fell ill. A defective hazardous waste treatment system and central air conditioning system would increase the likelihood of a lab employee (or several) becoming infected with SARS-CoV-2, as viral particles would be more likely to remain in the air for longer periods of time. As previously discussed, the WIV provides a shuttle for employees, transporting individuals from near the old WIV facility in Wuchang to the WNBL and back. The infected employees (whether from the WNBL or the WIV Headquarters) then traveled throughout central Wuhan, likely by the metro, spreading the virus.

In early September, it became known that an accidental release occurred. Initially, not knowing SARS-CoV-2 spreads via human-to-human transmission or that asymptotic people are responsible for a large number of new cases, concern was low. Concern was additionally tempered by the knowledge that previous accidental releases from labs resulted in only a small number of infections. Still, measures are ordered in response. At midnight local time on the morning of September 12th, the Wuhan University, which sits less than a mile from the WIV Headquarters and whose medical school houses a BSL-3 lab accredited to experiment on animals,[222] issues a notice for laboratory inspections in late September.[223] It is likely that officials issued similar orders to other labs in the area. Between two and three hours later, the WIV's viral sequence database is taken offline in the middle of the night.[224] Roughly 17 hours later, at 7:09 p.m. local time, the WIV publishes a procurement announcement for "security services" at the WNBL, to include gatekeepers, guards, video surveillance, security patrols, and people to handle the "registration and reception of foreign personnel."[225] The budget provided was in excess of $1.2 million.[226]

In order to prevent national embarrassment, the decision was made to allow the 2019 Military World Games to continue. No spectators were allowed to attend the games, but international athletes and some of the 236,000 volunteers still become infected, spreading the virus in the city. Dozens of athletes fall ill with symptoms. Since COVID-19 can infect humans without causing symptoms, an untold number of athletes and volunteers become infected, but are asymptomatic and unaware they are infectious.

The athletes return to their home countries in late October, carrying SARS-CoV-2 across the world. Just as was the case in 2002 with SARS,[227] the CCP sought to hide the outbreak, wasting precious time that could have been used to prevent the global pandemic. By the time the world was alerted to the virus spreading in Wuhan, it had already begun to spread around the world.

In December, as cases begin to overload local hospitals, it became impossible to hide the outbreak. At some point in late 2019, Major General Chen Wei is brought in to take over the BSL-4 lab at the WNBL and lead the response efforts. The Wuhan Branch of the China CDC set a case definition for COVID-19 that only included those who have visited the Huanan Seafood Market, meaning that only people who had a link to the market were identified as having COVID-19. This further obscured the true origins of the virus.

Linfa Wang, a scientist with ties to the WIV and who has worked with Shi, Hu, and Daszak on the genetic modification of coronaviruses, was in Wuhan in early January 2020. While there he visited the WIV and likely met with Shi, Hu, and others. Sometime after his departure on Januarty 18th and before February 6th, WIV researchers asked Peter Daszak to organize a public statement suppressing debate regarding the lab as the origin of SARS-CoV-2. On January 20th, WIV researchers submitted the February 2020 article where ID4991 was renamed as RaTG13 and which contained false information about when the genomic sequence for the virus was obtained.

At 12:43am on February 6th, Daszak sent the draft statement to Wang, Baric, and others asking them to join as cosigners. Sometime before Daszak went to bed that night, Wang called him and requested that he, Daszak, and Baric not sign the statement in order to obfuscate their connections to the WIV. Baric agreed, and neither him nor Wang signed the statement. The statement was published on February 19th, declaring discussion of a lab leak a conspiracy theory, and suppressing public debate on the origins of COVID-19.

220 "Notice of the Resource Allocation and Management Department of the Basic Research Department of the Ministry of Science and Technology on the Comprehensive Performance Evaluation of Special Projects of Basic Science and Technology Work." *Ministry of Science and Technology,* 4 July 2019. https://archive.is/pIwh4#selection-703.7-711.34

221 Ge.

222 "About Wuhan University School of Medicine (WUSM)." *Wuhan University School of Medicine,* 23 Apr. 2013, https://wsm70.whu.edu.cn/English_Site/About.htm

223 "Notice on the implementation of laboratory safety inspections in 2019." *Wuhan University,* http://simlab.whu.edu.cn/info/1107/1018.htm

224 "Status breakdown of the database of characteristic wild animals carrying virus pathogens (September 2019)." *Scientific Database Service Monitoring & Statistics System.* https://archive.is/AGtFv#selection-1553.0-1567.2

225 "Competitive consultation on the procurement project of security services in Zhengdian Science Park, Wuhan Institute of Virology, Chinese Academy of Sciences." China Government Procurement Network, 12 Sept. 2019, https://web.archive.org/web/20210716170719/http://www.ccgp.gov.cn/cggg/dfgg/jzxcs/201909/t20190912_12900712.htm

226 *Ibid.*

227 Epstein, Gady A. "Chinese Admit to SARS Mistakes." *Baltimoresun.com*, Baltimore Sun, 1 Apr. 2003, www.baltimoresun.com/bal-te.sars21apr21-story.html.

V. RECOMMENDATIONS

In the previously issued report, Committee Minority Staff provided several recommendations for actions to be taken by the United States in response to COVID-19, including seeking new leadership at the WHO, pursuing Taiwan's re-admittance to the WHO as an observer, engaging in an international investigation with likeminded WHO Member States regarding the early stages of COVID-19, and supporting concrete reforms to the International Health Regulations. These recommendations remain relevant.

In response to the new information laid out in this addendum, there are additional steps that can be taken by the Committee, Congress more broadly, and the Executive Branch on this issue. Given the previously detailed inconsistences and CCP disinformation campaign regarding a possible lab leak, Peter Daszak must be subpoenaed to appear before the House Foreign Affairs Committee and Senate Foreign Relations Committee as material witness to this investigation. Committee Minority Staff attempted, on multiple occasions, to contact Daszak with a list of questions relevant to this report. He never responded. In contrast, Ralph Baric provided answers to a list of questions from Committee Minority Staff. His assistance was appreciated, and we believe his testimony would also be useful. Daszak and Baric should provide expert testimony, including but not limited to the following questions:

- What was the extent of genetic manipulation of coronaviruses and their testing against human immune systems at the WIV in 2018 and 2019?
- Who requested the statement of support published in the *Lancet*?
- Did this request include labeling discussion of a possible lab leak as a conspiracy theory?
- What was the nature and content of Wang's call to Daszak in the early hours of February 6th, 2020?
- Why did Daszak make conflicting, and apparently false, statements regarding the NIH grant terminated in 2020?
- How could Daszak confirm RaTG13 is the closet match to SARS-CoV-2 in the WIV's database if it was taken offline in September 2019?
- Does Daszak have a copy of the WIV's database that was taken offline?
- Who put forth Daszak's name to join the joint WHO-China investigative team?
- Was Daszak aware the funding he was providing directly supported gain-of-function research by paying for the collection of viruses the WIV later experimented with, even though the federal government had a moratorium on such research from 2014 through 2017?
- Do they believe SARS-CoV-2 could possibly be a genetically modified virus created via a system similar toBaric's "no-see-um" method and the system used by WIV researchers in 2016, thus leaving no evidence of manipulation?

Committee Minority Staff also recommends Congress pursue legislation to implement the following restrictions and sanctions in response to the pandemic:

- Institute a ban on conducting and funding any work that includes gain-of-function research until an international and legally binding standard is set, and only where that standard is verifiably being followed.
- Authorize and fund a public-private partnership for pandemic prevention, warning, and early detection.

- Sanction the Chinese Academy of Sciences and affiliated entities.
- List the Wuhan Institute of Virology and its leadership on the Specially Designated Nationals and Blocked Persons List and apply additional, appropriate secondary sanctions.
- Expand statutory and administrative sanctions regimes to curb the abuse of dual-use technology.
- Authorize new sanctions for academic, governmental, and military bioresearch facilities that fail to ensure the appropriate levels of safety and information sharing.
- Review all H-2B visas of Chinese nationals engaged in biological, chemical, or related research in the United States for possible revocation.
- Review all student visas of Chinese nationals studying at U.S. academic institutions for possible revocation.

Additionally, the Executive Branch should engage in international negotiations to establish a legally binding international standard for laboratory biosafety, to include certification and inspections by an international organization similar to the International Atomic Energy Agency.

Foreign governments facing economic contraction that have entered into agreements under the PRC's Belt and Road Initiative are encouraged to examine bilateral agreement terms. In particular, agreements or memoranda of understanding that promote joint scientific and academic research wherein the Chinese government has access to natural resources, minerals, plant life, and animals unique to the nation state. Agreements that promote adaptation of governing structures that centralize control over all local, municipal, or provincial levels increase the risk of creating national governing structures that manipulate, misinform, misdirect and gaslight their own citizens to protect centralized governing structures.

Foreign governments considering entering into bilateral agreements with the PRC are advised to be aware that based on the information presented within this report, the PRC conducts scientific research without regard for adequate safety protocols in place, in a manner that does not comport with international safety standards, and without adequate assessment of the risks scientific research may pose to the environment, test subjects, or humanity. It is the recommendation of the Committee Minority Staff that such agreements be avoided.

VII. CONCLUSION

The Intelligence Community 90-day review report on the origins of COVID-19, ordered by President Biden, is due no later than August 24, 2021. While based on open source information, it is the hope of Committee Minority Staff that the collection and analysis contained within this addendum, produced at the direction of Ranking Member Michael T. McCaul, will help inform the public debate about the viability of a laboratory accident being the source of SARS-CoV-2. It is vital the public discourse surround the Wuhan Institute of Virology is transparent, honest, and detailed.

It is the opinion of Committee Minority Staff, based on the preponderance of available information; the documented efforts to obfuscate, hide, and destroy evidence; and the lack of physical evidence to the contrary; that SARS-CoV-2 was accidentally released from a Wuhan Institute of Virology laboratory sometime prior to September 12, 2019. The virus, which may be natural in origin or the result of genetic manipulation, was likely collected in the identified cave in Yunnan province, PRC, sometime between 2012 and 2015. Its release was due to poor lab safety standards and practices, exacerbated by dangerous gain-of-function research being conducted at inadequate biosafety levels, including BSL-2. The virus was then spread throughout central Wuhan, likely via the Wuhan Metro, in the weeks prior to the Military World Games. Those games became an international vector, spreading the virus to multiple continents around the world.

It is incumbent on the parties identified in this report to respond to the issues raised herein and provide clarity and any new or additional evidence as soon as possible. As always, Committee Minority Staff stands ready to receive such evidence or testimony that supports or contradicts this report. Until such time as the Chinese Communist Party lifts its self-imposed veil of secrecy, explains its lies regarding the early stages of the pandemic, and provides access to the WIV’s archives and sample database, questions will remain as to the origins of SARS-CoV-2 and the COVID-19 pandemic. Until that day, it is incumbent upon the United States and likeminded countries around the world to ensure accountability, and implement the reforms necessary to prevent the CCP’s malfeasance from giving rise to a third pandemic during the 21st century.

VII. APPENDIX

Timeline of the WIV Lab Leak and the Start of the COVID-19 Pandemic

April 2012: Six miners working in a copper mine located in a cave in Yunnan province of the PRC fall ill. Between the ages of 30 and 63, the workers presented to a hospital in Kunming with persistent coughs, fevers, head and chest pains, and breathing difficulties." Three of the six died.

Late 2012 – 2015: Researchers from the WIV collect samples from bats in the cave.

2015 - 2017: Shi Zheng-li, Ben Hu, Peter Daszak, and Linfa Wang jointly publish research on the isolation of novel coronaviruses. They conduct gain-on-function research, testing novel and genetically manipulated coronaviruses against mice and other animals expressing human immune systems. At times they collaborate with Ralph Baric.

2018 – 2019: Shi, Hu, and other researchers at the WIV infect transgenic mice and civets expressing human immune systems with unpublished novel and genetically modified coronaviruses.

July 4, 2019: The PRC's Ministry of Science and Technology orders a review of several grants, including grant no. 2013FY113500. This is the grant which funded the collection of hundreds of coronaviruses and bat samples from the cave in Yunnan province.

July 16, 2019: The WIV publishes a tender requesting bids to conduct renovation on the hazardous waste treatment system at the Wuhan National Biosafety Lab (WNBL). The closing date was July 31st.

Late August/Early September 2019: One or more researchers become accidently infected with SARS-CoV-2, which was either collected in the Yunnan cave, or the result of gain-of-function research at the WIV. They travel by metro in central Wuhan, spreading the virus.

September 12, 2019: At 12:00am local time, the Wuhan University issues a statement announcing lab inspections. Between 2:00am and 3:00am, the WIV's viral sequence and sample database is taken offline. At 7:09pm, the WIV publishes a tender requesting bids to provide security services at the WNBL.

September – October 2019: Car traffic at hospitals surrounding the WIV Headquarters, as well as the shuttle stop for the WNBL, show a stead increase before hitting its highest levels in 2.5 years. Baidu search terms for COVID-19 related symptoms increase in a corresponding manner.

Late October – Early November 2019: The international athletes return home, carrying SARS-CoV-2 around the world.

November 21, 2019: A 4-year-old boy from Milan, Italy develops a cough. His samples will later test positive for COVID-19.

November 27, 2019: Samples of wastewater are collected in Brazil that will later test positive for the presence of SARS-CoV-2 RNA.

December 1, 2019: The CCP's first "official" case of COVID-19 become infected.

Late 2019: Major General Chen Wei arrives in Wuhan, taking over the WNBL BSL-4 lab.

Dec. 27, 2019: A Chinese genomic company reportedly sequenced most of the virus in Wuhan and results showed a similarity to SARS. Zhang Jixian, a doctor from Hubei Provincial Hospital of Integrated Chinese and Western Medicine, tells PRC health authorities that a novel disease affecting some 180 patients was caused by a new coronavirus.

Dec. 29, 2019: Wuhan Municipal CDC organized an expert team to investigate after the Hubei Provincial Hospital of Integrated Chinese and Western Medicine and other hospitals find additional cases.

Dec. 30, 2019: Doctors in Wuhan report positive tests for "SARS Coronavirus" to local health officials. Under the 2005 International Health Regulations, the PRC is required to report these results to the WHO within 24 hours. They do not.

Dec. 31, 2019: WHO officials in Geneva become aware of media reports regarding an outbreak in Wuhan and direct the WHO China Country Office to investigate.

Jan. 2020: Linfa Wang meets with collaborators at the WIV, likely including Shi and Hu.

Jan. 1, 2020: Hubei Provincial Health Commission official orders gene sequencing companies and labs who had already determined the novel virus was similar to SARS to stop testing and to destroy existing samples. Dr. Li Wenliang is detained for "rumor mongering."

Jan. 2, 2020: The Wuhan Institute of Virology (WIV) completes gene sequencing of the virus, but the CCP does not share the sequence or inform the WHO. PRC aggressively highlights the detentions of the Wuhan doctors.

Jan. 3, 2020: China's National Health Commission ordered institutions not to publish any information related to the "unknown disease" and ordered labs to transfer samples to CCP controlled national institutions or destroy them.

Jan. 11-12, 2020: After a researcher in Shanghai leaks the gene sequence online, the CCP transmits the WIV's gene sequencing information to the WHO that was completed 10 days earlier. The Shanghai lab where the researcher works is ordered to close.

Jan. 14, 2020: Xi Jinping is warned by a top Chinese health official that a pandemic is occurring.

Jan. 18, 2020: Linfa Wang departs Wuhan.

Jan. 20, 2020: WIV researchers submitted an article claiming that SARS-CoV-2 is natural in origin. The article renames ID4991 as RaTG13 and contained false information about when the genomic sequence for the virus was obtained.

Jan. 23, 2020: The CCP institutes a city-wide lockdown of Wuhan. However, before the lockdown goes into effect, an estimated 5 million people leave the city.

Last Week of January 2020: Daszak and other outside experts edit a letter to be sent by the Presidents of the National Academies of Sciences, Engineering, and Medicine to the White House Office of Science and Technology Policy. Daszak pushes for language to address "conspiracy theories."

Jan. 30, 2020: One week after declining to do so, Tedros declares a Public Health Emergency of International Concern.

Late Jan. – Early Feb. 2020: PRC researchers, likely those at the WIV, request Peter Daszak's assistance in responding to suggestions of a lab leak or genetic manipulation of SARS-CoV-2. Daszak helps edit the National Academies of Sciences, Engineering, and Medicine's response to the White House Office of Science and Technology Policy on the origins of COVID-19.

Feb. 3, 2020: The WIV researchers' paper submitted on January 20th is published by *Nature* online.

Feb. 6, 2020 at 12:43:40 am: Daszak sends the draft Lancet statement, which cites the Feb. 3 WIV paper, to Wang, Baric, and others asking them to join as cosigners. Within hours, Wang calls him, informs Daszak that he will not sign, and requests that neither Daszak or Baric sign.

Feb. 6, 2020 (Afternoon): At 3:16pm, Daszak send a High Important email to Baric, forwarding Wang's request, and informing Baric the statement will be "put out in a way that doesn't link it back to our collaboration." At 4:01:22 pm, Baric agrees to not sign the statement.

Feb. 7, 2020: Dr. Li, who first shared the positive SARS test results with his classmates via WeChat, dies from COVID-19.

Feb. 9, 2020: The death toll for COVID-19 surpasses that of SARS.

Feb. 15, 2020: First death from COVID-19 outside of Asia occurs, in France.

- **Feb. 16, 2020:** WHO and PRC officials begin a nine-day "WHO-China Joint Mission on Coronavirus Disease 2019" and travel to the PRC to examine the outbreak and origin of COVID-19. Many team members, including at least one American, were not allowed to visit Wuhan.
- **Feb. 18, 2020:** Daszak statement is published by the *Lancet* online, which references the letter from the U.S. National Academies of Sciences, Engineering, and Medicine he helped write and the WIV's February 3rd paper on the origins of COVID-19. Despite drafting the letter, Daszak is not listed as the corresponding author.
- **Feb. 25, 2020:** For the first time, more new cases are reported outside of PRC than within.
- **Feb. 26, 2020:** The WHO-China Joint Mission issues its findings, praising the PRC for its handling of the outbreak.
- **Feb. 29, 2020:** The first reported COVID-19 death in the United States occurs.
- **March 11, 2020:** The WHO officially declares the COVID-19 outbreak a pandemic after 114 countries had already reported 118,000 cases including more than 1,000 in the United States.
- **Nov. 17, 2020:** As a result of public pressure, Shi, Hu, and other WIV researchers publish an addendum to their February 3rd paper, confirming that RaTG13 was ID4991 collected from the cave in Yunnan, and revealing they collected 293 coronaviruses from the cave between 2012 and 2015.
- **June 15, 2021:** The Presidents of the U.S. National Academies of Sciences, Engineering, and Medicine release a statement saying, "let scientific evidence determine origin of SARS-CoV-2."
- **June 21, 2021:** After public pressure, Daszak updates his public disclosure form for the *Lancet* statement. He does not mention the WIV or that the statement was drafted at the request of PRC researchers.
- **July 5, 2021:** Daszak and 23 of the original 27 authors release an update to their February 2021 statement, walking back their labeling of public debate around the source of the virus as "conspiracy theories."

China Center for Disease and Control Memo on Supplementary Regulations

中国疾控中心处(室)便函

科技处便函〔2020〕16 号

关于加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定

中心直属各单位，机关各处室：

为进一步加强我中心新型冠状病毒肺炎应急响应期间科研管理，根据上级有关文件精神，特制定《加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定》，请各单位和各处室负责人务必高度重视，层层传达，必须通知到每个人。如有违反有关规定者，将追究单位和违规者的责任。

附件：加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定

中国疾控中心科技处

2020 年 2 月 25 日

抄送：高福、李新华、刘剑君、冯子健。

附件

加强新型冠状病毒肺炎应急响应期间有关科技管理的补充规定

根据《国家卫生健康委办公厅关于在重大突发传染病防控工作中加强生物样本资源及相关科研活动管理工作的通知》(国卫办科教函〔2020〕3 号)、《科技部办公厅关于加强新型冠状病毒肺炎科技攻关项目管理有关事项的通知》等文件精神，为有力抗击新型冠状病毒肺炎(简称“新冠肺炎”)疫情，严格规范科研管理，进一步加强科研管理制度的落实，现对《加强新型冠状病毒感染的肺炎应急响应期间有关科技管理规定》(中疾控科技便函〔2020〕128 号)制定本补充规定。

一、坚持国家和人民利益至上，以做好新冠肺炎疫情防控为首要任务。疫情应急响应期间，要集中优势力量，分清轻重缓急，将主要精力放在疫情防控中，把论文“写在祖国大地上”，把研究成果应用到战胜疫情中，在疫情防控任务完成之前不应将精力放在论文发表上。

二、开展新冠肺炎疫情相关科研项目，必须经科技组/科技处进行初审，根据研究内容组织专家进行科学论证和伦理审查，必要时提请应急领导小组或国家卫生健康委科教司审批。上级委托的科研项目必须经科技组/科技处请示应急领导小组审定并备案。

三、任何人不能以个人或研究团队名义擅自向其他机构和个人提供新冠肺炎疫情相关信息，包括数据、生物标本、病原体、培养物等。

四、在发表与新冠肺炎疫情相关的论文和成果前，必须先报科技组/科技处初审，必要时提请应急领导小组或国家卫生健康委科教司审批。

未经科技组/科技处审核的已投稿的论文，尽快撤稿并执行本规定。

五、科研项目进展报告原则上按月报科技组/科技处，或根据上级要求的时限进行报告。

六、要严格遵循医学伦理、科研诚信和学风建设等相关规定。

七、有违反上述规定者，依纪依法依规进行严肃处理。

八、本规定发布之日执行，由科技组/科技处解释。

中国疾控中心科技处

2020 年 2 月 25 日

Memo to the Offices of the Chinese Center for Disease Control and Prevention

Memo (2020) No. 16 of the Science and Technology Department

On the Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia

All units and offices directly under the center:

In order to further strengthen scientific research management in our center during the emergency response to the novel coronavirus pneumonia, and in accordance with the spirit of relevant documents issued by the higher authorities, the "Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia" has been formulated. Every unit and office, please attach great importance to it and spread it through all levels - everyone must be notified. In case of any violation of relevant regulations, the offender and their unit will be held accountable.

Attachment: Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia

Chinese Center for Disease Control and Prevention

February 25, 2020

CC: Gao Fu, Li Xinhua, Liu Jianjun, Feng Zijian.

Annex

Supplementary Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia

According to the spirit of the "Notice of the General Office of the National Health Commission on Strengthening the Management of Biological Sample Resources and Related Scientific Research Activities during the Prevention and Control of Major Infectious Diseases" (National Health Commission Science and Technology Memo [2020] No. 3), the "Notice of the General Office of the Ministry of Science and Technology on Strengthening the Management of New Coronavirus Pneumonia Science and Technology Research Projects" and other documents, and in order to effectively combat the new coronavirus pneumonia ("COVID-19") epidemic, to strictly standardize scientific research management, and to further strengthen the implementation of scientific research management systems, these supplementary "Regulations on Strengthening the Management of Science and Technology During the Emergency Response to the Novel Coronavirus Pneumonia" (Chinese Center for Disease Control Science and Technology Memo [2020] No. 128) have been formulated.

1. Prioritize the interests of the country and the people and take the prevention and control of the COVID-19 epidemic as the primary task. During the emergency response against the epidemic, we must concentrate our forces, distinguish our priorities, focus our main energies on controlling the epidemic, write papers "on the land of the motherland", apply research results to the fight against the epidemic, and not focus on publishing papers until the epidemic is under control.

2. The launch of scientific research projects related to the COVID-19 epidemic must undergo preliminary review by the Science and Technology Group/Department. According to the research subject, experts should be organized to conduct scientific and ethical reviews, and, if necessary, the project must be submitted to the emergency

leading group or the Department of Science and Education of the National Health Commission for approval. The research projects authorized by higher authorities must be examined and approved by the emergency leading group via the Science and Technology Group/Department and be kept on record.

3. No one can, under their own name or in the name of their research team, provide other institutions and individuals with information related to the COVID-19 epidemic on their own, including data, biological specimens, pathogens, culture, etc.

4. Before publishing papers and research results related to the COVID-19 epidemic, you must first report them to the Science and Technology Group/Department for preliminary review, and if necessary, submit it to the Emergency Leading Group or the Department of Science and Education of the National Health Commission for approval.

Papers that have been submitted but not yet reviewed by the Science and Technology Group/Department should be withdrawn as soon as possible and redone according to these regulations.

5. In principle, progress reports on scientific research projects should be reported to the Science and Technology Group/Department on a monthly basis, or according to the time period stipulated by higher authorities.

6. Strictly follow relevant regulations on medical ethics, scientific research integrity and academic spirit.

7. Anyone who violates the above regulations shall be dealt with severely in accordance with discipline, laws and regulations.

8. The date of the implementation of this regulation will be explained by the Science and Technology Group/Department.

Chinese Center for Disease Control and Prevention

February 25, 2020

JCPM Confidential Notice on the Standardization of the Management of Publication of Novel Coronavirus Pneumonia Scientific Research

国务院应对新型冠状病毒肺炎疫情联防联控机制科研攻关组

关于规范新冠肺炎科研攻关成果信息发布管理的通知

国务院应对新型冠状病毒肺炎疫情联防联控机制科研攻关组成员单位办公厅(室)，有关单位：

为深入贯彻国务院应对新型冠状病毒肺炎疫情联防联控机制(以下简称国务院联防联控机制)会议的有关要求，切实规范科研攻关成果信息发布管理，现就有关事项通知如下。

一、全面加强科研攻关成果信息发布管理

按照“依法依规、科学客观、归口管理、精准发布”的原则，把新冠肺炎治疗药物、疫苗、病毒溯源、病毒传播途径、检测试剂等各类疫情防控科研成果信息的发布工作，纳入国务院应对新型冠状病毒肺炎疫情联防联控机制科研攻关组(以下简称科研攻关组)的统一部署。科研攻关组统筹协调科研应急攻关成果信息发布，指导、协调各地各单位科研成果信息发布。

二、建立规范的科研攻关成果信息发布机制

科研攻关组各成员单位及时汇总本单位、本系统科研攻关成果信息，就发布内容，发布形式进行审核把关，并及时报科研攻关组批准。科研攻关组按业务归口组织各专班负责对发布内容、发布形式提出专业性审核意见，必要时组织专家论证。科研攻关组同意后，发布单位应根据工作需要选择新闻发布会、官方网站、政务新媒体、新闻媒体等平台发布，并通报国务院联防联控机制宣传组、科研攻关组。原则上，新冠肺炎科研成果信息首发采用官方权威发布形式。舆论专班加强与宣传组沟通，结合舆情动态和社会关切，强化对科研成果信息发布的指导。

三、严格要求各科研单位做好科研成果信息发布

联防联控机制科研攻关组各成员单位要按照归口管理原则，严格本单位本系统相关科研成果信息的发布审批程序，加强对本单位本系统归口管理的高等院校、研究机构、企业的管理，将本通知要求传达至从事新冠肺炎研究的各相关单位。各成果信息发布单位是发布内容的第一责任人，要综合考虑实际工作进展、疫情防治态势、社会关切问题、预期发布成效等方面，精准确定发布内容，合理引导社会预期。各高等院校、研究机构、医疗机构、企业及其人员在疫情防控期间，未经审批不得擅自发布疫情防控相关科研成果信息。在中华医学会平台交流的论文仍按原备案机制办理。

四、加强科研攻关成果信息发布工作统筹

疫情防控期间，各地各单位要认真贯彻落实习近平总书记关于疫情防控工作的一系列重要指示精神，进一步强化大局意识、责任意识，加强审核把关，主动沟通协调，形成新冠肺炎科研成果信息发布全国“一盘棋”格局。重要敏感科研成果信息要反复核实，把握不准的要及时按程序向科研攻关组及相关部门请示。

五、强化监督问责

对未按规定程序报批，发布未经证实的虚假科研成果信息，造成严重不良社会影响的，要追究责任。

联系人：赵 婧，[redacted]、[redacted]

吴运高，[redacted]、[redacted]

传真：[redacted]，联系邮箱：[redacted]

国务院应对新型冠状病毒肺炎
疫情联防联控机制科研攻关组
（代章）
2020 年 3 月 3 日

(此件不公开)

抄送：国务院联防联控机制宣传组。

科学技术部办公厅　　2020 年 3 月 3 日印发

Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia Scientific Research Group

Notice on the Standardization of the Management of Publication of Novel Coronavirus Pneumonia Scientific Research

To the Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia member work units and offices, and other relevant work units:

In order to thoroughly implement relevant requirements from the meeting of the Joint Prevention and Control Mechanism of the State Council in Response to the Novel Coronavirus Pneumonia (hereinafter referred to as the "Joint Prevention and Control Mechanism of the State Council"), and to effectively standardize the management of the publication of scientific research, the following is issued below.

1. Comprehensively strengthen the management of publication of scientific research

In accordance with the principles of "following laws and regulations, being scientific and objective, centralized management, and precise publications", all publication work on epidemic prevention research and information related to COVID-19, including medication, vaccines, virus origins, virus transmission routes, testing reagents, etc. will be taken over by the Joint Prevention and Control Mechanism of the State Council's scientific research group (hereinafter referred to as "the scientific research group") for coordinated deployment. The scientific research group will coordinate the publication of information on emergency scientific research, and guide and coordinate the publication of information on scientific research by all work units in all locations.

2. Establish a standardized publication mechanism for scientific research

Each member work unit of the scientific research team will gather scientific research information within their own unit and systems, review and check the content and form of its publication, and report it to the scientific research team for approval in a timely manner. The scientific research group's dedicated teams of professionals and various experts are responsible for reviewing the publication's content and format and giving expert opinions, and when necessary, arranging expert assessment. After the scientific research group approves, the publishing work unit should, according to work requirements, arrange publication via press conferences, official websites, state social media, news media and other platforms, and notify the propaganda and scientific research teams of the Joint Prevention and Control Mechanism of the State Council. In principle, COVID-19 scientific research should be published first in the form of an official authoritative publication. The special group on public opinion should strengthen communication with the propaganda team, take into account the trend of public opinion and social concerns, and strengthen guidance of the publication of scientific research and information.

3. Strictly require all scientific research units to do a good job on the publication of scientific research

The member work units of the scientific research team of the Joint Prevention and Control Mechanism shall follow the principle of centralized management, strictly enforce their own system's publication approval procedures for relevant scientific research, strengthen the management of universities, research institutions, and enterprises under the centralized management of their work unit systems, and communicate the requirements of this notice to all relevant units engaged in research on COVID-19. The publishing work unit is the one primarily responsible for the research content they publish, and they must consider, in a comprehensive manner, the research progress, the epidemic prevention and control situation, societal concerns, the consequences of publication, and various other issues. They must ensure the accuracy of the published content and guide societal expectations in a reasonable manner. During the period of epidemic prevention and control, all universities, research institutions, medical institutions, enterprises and their staff shall not publish information on scientific research related to epidemic prevention and control without approval. Papers exchanged on the Chinese Medical Association

四、加强科研攻关成果信息发布工作统筹

疫情防控期间，各地各单位要认真贯彻落实习近平总书记关于疫情防控工作的一系列重要指示精神，进一步强化大局意识、责任意识，加强审核把关，主动沟通协调，形成新冠肺炎科研成果信息发布全国“一盘棋”格局。重要敏感科研成果信息要反复核实，把握不准的要及时按程序向科研攻关组及相关部门请示。

五、强化监督问责

对未按规定程序报批，发布未经证实的虚假科研成果信息，造成严重不良社会影响的，要追究责任。

联系人：赵 婧，[redacted]、[redacted]

吴运高，[redacted]、[redacted]

传真：[redacted]，联系邮箱：[redacted]

国务院应对新型冠状病毒肺炎
疫情联防联控机制科研攻关组
（代章）
2020 年 3 月 3 日

(此件不公开)

抄送：国务院联防联控机制宣传组。

科学技术部办公厅　　2020 年 3 月 3 日印发

February 6, 2020, Email at 12:43am from Peter Daszak to Ralph Baric, Linfa Wang, and Others Inviting Them to Sign the Statement

A Statement in support of the scientists, public health and medical professionals of China

Feb 6, 2020 12:43:40 AM EST

A Statement in support of the scientists, public health and medical professionals of China

Subject:	A Statement in support of the scientists, public health and medical professionals of China
From:	Peter Daszak [redacted]
To:	Ralph Baric [redacted]
Cc:	[redacted]
Sent:	February 6, 2020 12:43:40 AM EST
Attachments:	Statement of support, 2019nCoV China Final.docx

A Statement in support of the scientists, public health and medical professionals of China

Feb 6, 2020 12:43:40 AM EST

Dear Ralph, Linda, Jim, Rita, Linfa and Hume,

I've been following the events around the novel coronavirus emergence in China very closely and have been dismayed by the recent spreading of rumors, misinformation and conspiracy theories on its origins. These are now specifically targeting scientists with whom we've collaborated for many years, and who have been working heroically to fight this outbreak and share data with unprecedented speed, openness and transparency. These conspiracy theories threaten to undermine the very global collaborations that we need to deal with a disease that has already spread across continents.

We have drafted a simple statement of solidarity and support for scientists, public health and medical professionals of China, and would like to invite you to join us as the first signatories. If you agree, we will send this letter to a group of around half-a-dozen other leaders in the field and then disseminate this widely with a sign-up webpage for others to show their support by signing up to its language. I will then personally present this at my plenary during the ICID 2020 conference in Malaysia in two weeks, with the goal of also getting widespread attention in SE Asia to our support for the work that our colleagues in China are undertaking.

I sincerely hope you can join us. Please review the letter, and let me know if you are willing to join Billy Karesh and myself as co-signatories. Also, please confirm your title and affiliation that will be shown in the letter. We plan to make circulate this widely to coincide with a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, which will likely be released tomorrow or Friday.

Thank you for your consideration and support of the scientific and public health community around the world!

Cheers,

Peter

Peter Daszak
President

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EcoHealth Alliance leads cutting-edge research into the critical connections between human and wildlife health and delicate ecosystems. With this science we develop solutions that prevent pandemics and promote conservation.

A Statement in support of the scientists, public health and medical professionals of China

Feb 6, 2020 12:43:40 AM EST

Statement in Support of the Scientists, Public Health, and Medical Professionals of China Combating the Novel Coronavirus Outbreak

We, the undersigned, are scientists who have followed the emergence of 2019-nCoV, and are deeply concerned about its global impact on people's health and well-being. We have watched as the scientists, public health and medical professionals of China have worked heroically to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. We sign this statement in solidarity with all scientists, public health, and medical professionals in China who continue to save lives and protect *global* health during the challenge of this novel coronavirus outbreak. We want you to know that we are all in this together, with you in front of us on the battlefield against the novel coronavirus.

The rapid, open and transparent sharing of data on 2019-nCoV is now being threatened by rumors and misinformation around the origins of this outbreak. We stand together to strongly condemn conspiracy theories suggesting that 2019-nCoV does not have a natural origin. Scientific evidence overwhelmingly suggests that this virus originated in wildlife, as have so many other emerging diseases (*1-4*). This is further supported by a letter from the Presidents of the US National Academies of Science, Engineering, and Medicine, and by the scientific communities they represent (INSERT REF). Conspiracy theories will do nothing but create fear, rumors, and prejudice that jeopardize our global collaboration in the fight against this virus. We need to prioritize scientific evidence and unity over misinformation and conjecture now. We want you all to know that **we stand with you**, the science and health professionals of China, in your fight against this virus.

We invite others to join us in supporting the scientists, public health, and medical professionals of Wuhan and across China. Stand with our colleagues on the front-line!

Please add your name in an act of support by going to [INSERT LINK HERE].

A Statement in support of the scientists, public health and medical professionals of China

Feb 6, 2020 12:43:40 AM EST

Signatories

Dr. Peter Daszak, President, EcoHealth Alliance
Dr. Jim Hughes, Professor Emeritus, Emory University
Dr. Rita Colwell, former Director of National Science Foundation
Dr. Ralph Baric, Professor, The University of North Carolina, Chapel Hill
Dr. Linda Saif, Distinguished University Professor, The Ohio State University
Dr. Billy Karesh, Executive Vice President, EcoHealth Alliance
Dr. Linfa Wang, Professor, Duke-NUS Medical School
Dr. Hume Field, Honorary Professor, The University of Queensland

References

1. P. Zhou *et al.*, A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, (2020).
2. R. Lu *et al.*, Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*, (2020).
3. N. Zhu *et al.*, A Novel Coronavirus from Patients with Pneumonia in China, 2019. *New England Journal of Medicine*, (2020).
4. L. Ren *et al.*, Identification of a novel coronavirus causing severe pneumonia in human: a descriptive study. *Chin Med J. Epub ahead of print*, (2020).

February 6, 2020, Email at 3:16pm from Peter Daszak to Ralph Baric Relaying Wang's Request Not to Sign the Statement

To: Peter Daszak [redacted]
Cc: [redacted]
From: Baric, Ralph [redacted]

Sent: Thur 2/6/2020 4:01:22 PM (UTC-05:00)
Subject: RE: No need for you to sign the "Statement" Ralph!!

I also think this is a good decision. Otherwise it looks self-serving and we lose impact. ralph

From: Peter Daszak [redacted]
Sent: Thursday, February 6, 2020 3:16 PM
To: Baric, Ralph S [redacted]
Cc: [redacted]
Subject: No need for you to sign the "Statement" Ralph!!
Importance: High

I spoke with Linfa last night about the statement we sent round. He thinks, and I agree with him, that you, me and him should not sign this statement, so it has some distance from us and therefore doesn't work in a counterproductive way.

Jim Hughes, Linda Saif, Hume Field, and I believe Rita Colwell will sign it, then I'll send it round some other key people tonight. We'll then put it out in a way that doesn't link it back to our collaboration so we maximize an independent voice.

Cheers,

Peter

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President

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February 8, 2020, Email at 8:52pm from Peter Daszak to Rita Colwell Alleging WIV Researchers Requested the Statement

From: Peter Daszak [redacted]
Sent: Saturday, February 08, 2020 8:52 PM
To: Rita Colwell [redacted]
Cc: Rita Colwell [redacted]
Subject: RE: coronavirus statement
Importance: High

Hi Rita,

I appreciate your comments and I think at this point, that work has already been done, with >50 genomes published from 12 countries, and phylogenetic analyses published by authors from multiple countries. I've tried to make this a bit more clear, and have edited the letter as follows, so it hopefully addresses your comments:

1) I've inserted a reference to the GISAID webpage where 57 (to date) full genome sequences of 2019-nCoV from 12 countries are published and analyzed

2) I've inserted a reference to the CDC webpage on 2019-nCoV which makes the following statement, completely in concurrence with our letter:

"2019-nCoV is a betacoronavirus, like MERS and SARs, both of which have their origins in bats. The sequences from U.S. patients are similar to the one that China initially posted, suggesting a likely single, recent emergence of this virus from an animal reservoir."

In addition, please note that we will not be referring to this as a 'petition' but as a 'statement in support of' – This is in the title and will be in all materials we send out. This is to avoid the appearance of a political statement – this is simply a letter from leading scientists in support of other scientists and health professionals who are under serious pressure right now.

I hope you are willing to sign on to this - your voice will be very influential, particularly in keeping these critical bridges open between the USA and China. You should know that the conspiracy theorists have been very active, targeting our collaborators with some extremely unpleasant web pages in China, and some have now received death threats to themselves and their families. They have asked for any show of support we can give them.

As soon as we hear back from you we'll get ready to send this to our larger list (attached), but of course if you don't feel comfortable, I'll make sure your name is not associated with this.

Cheers,

Peter

Peter Daszak
President

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